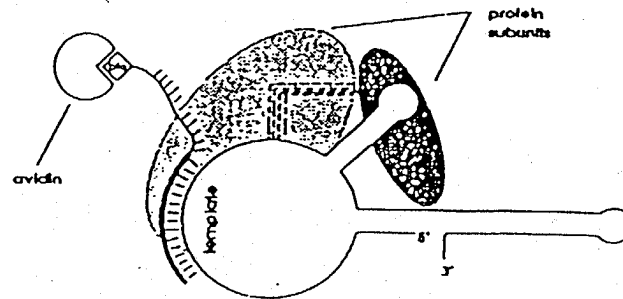


FIGURE 1

PANEL A



PANEL B

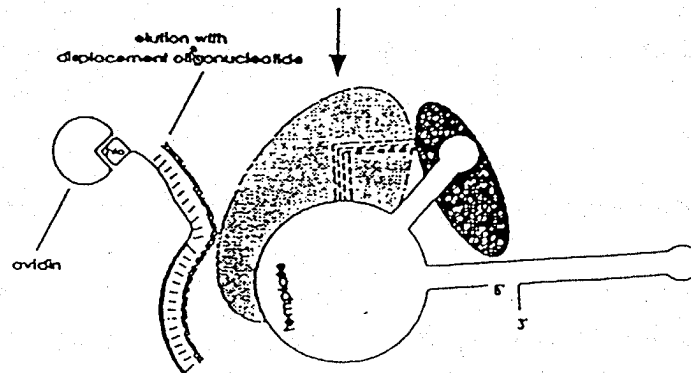


FIGURE 2

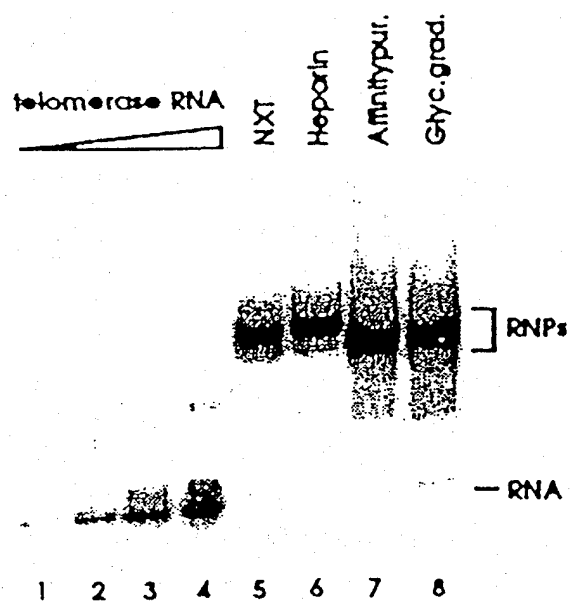


FIGURE 3

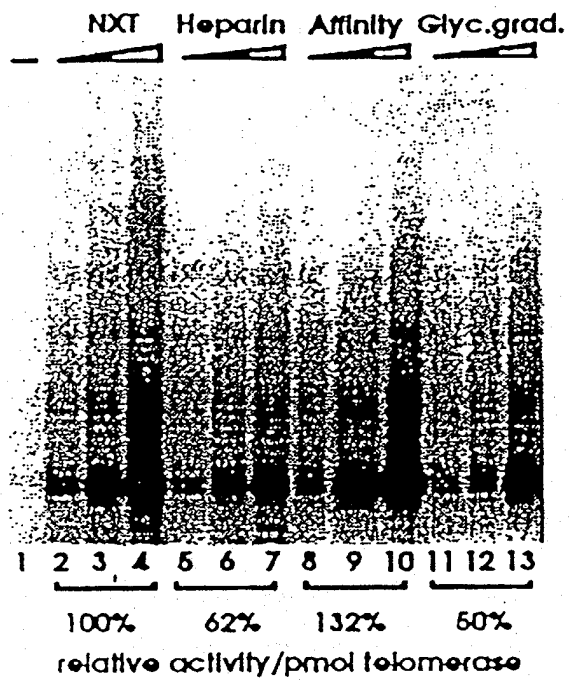


FIGURE 4

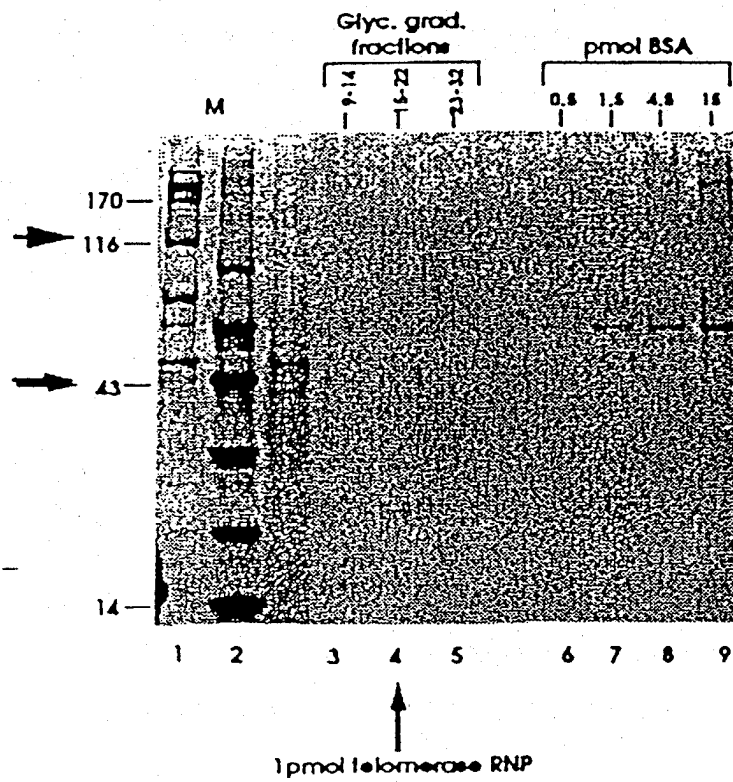


FIGURE 5

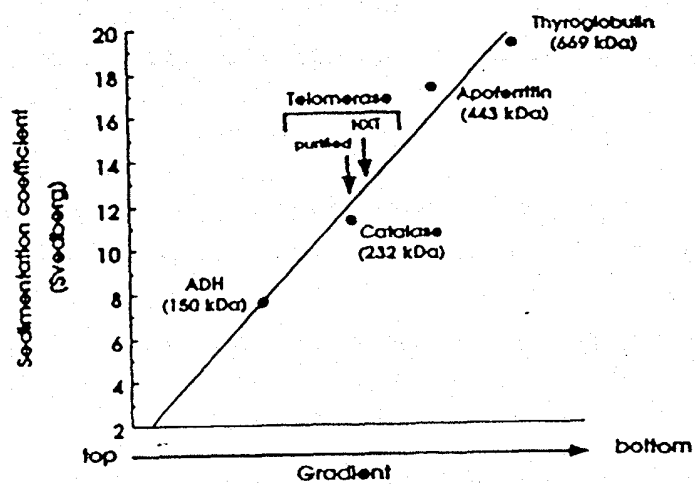
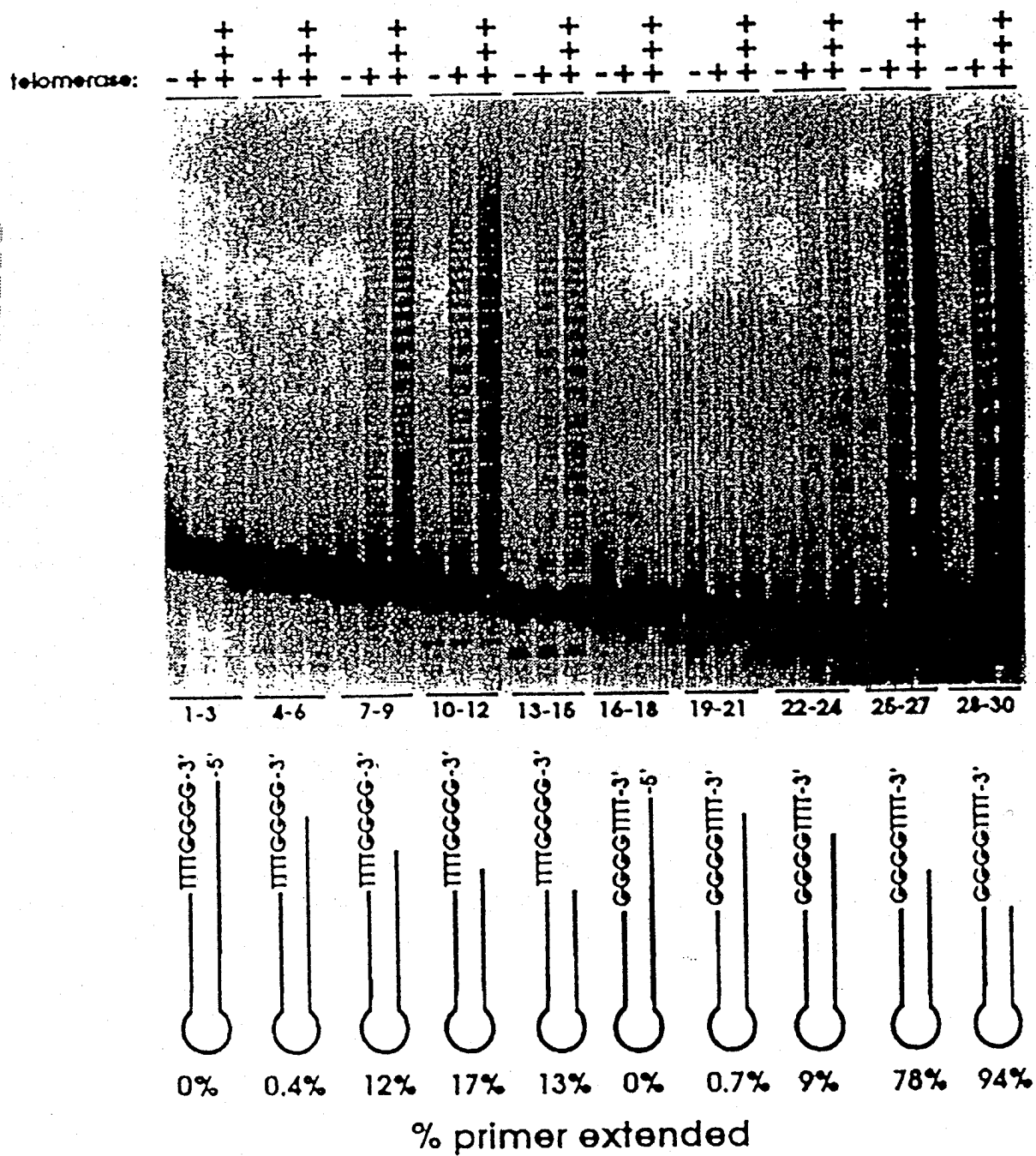


FIGURE 6



095653-0100

FIGURE 7

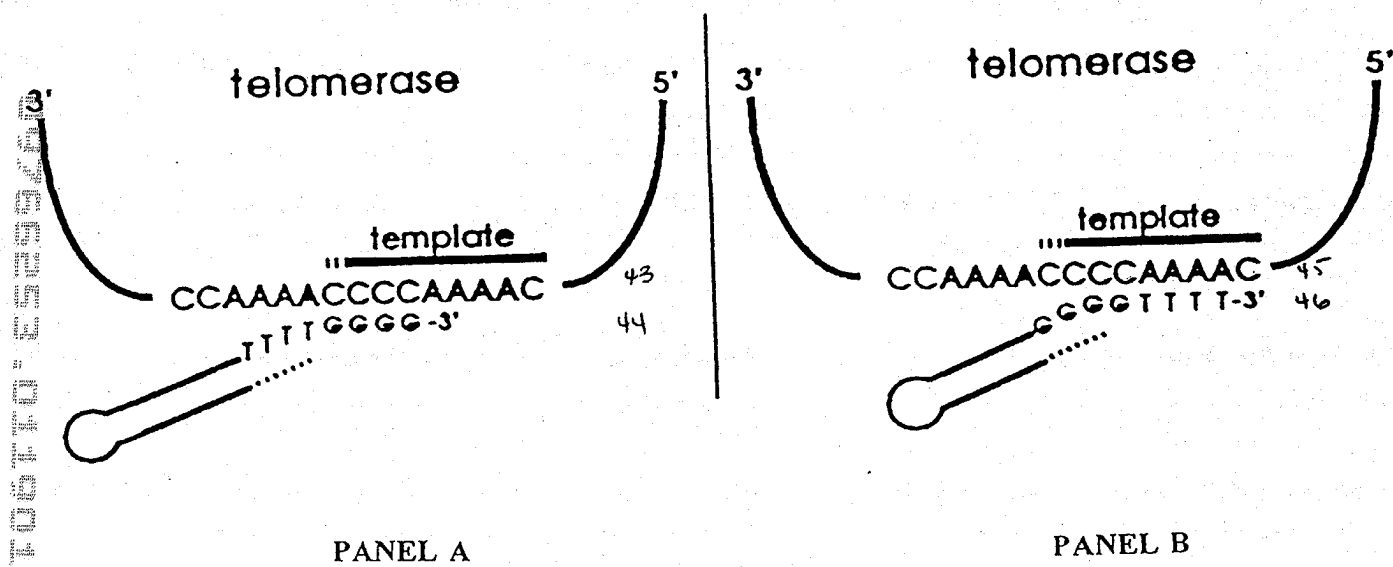
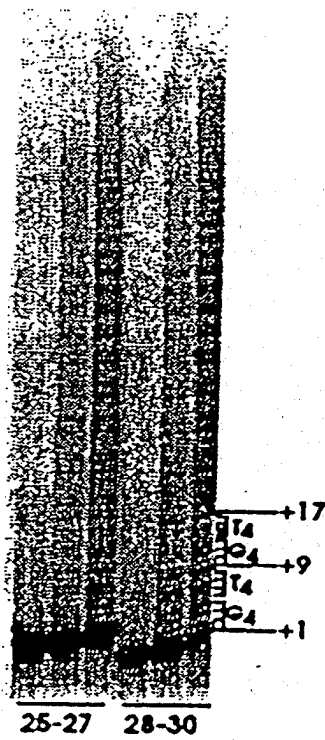


FIGURE 8



FOOTNOTES



FIGURE 9

1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT  
 51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA  
 101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC  
 151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA  
 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT  
 251 TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG  
 301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT  
 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT  
 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTC  
 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA  
 501 CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG  
 551 ATTGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA  
 601 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG  
 651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA  
 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA  
 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA  
 801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT  
 851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT  
 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA  
 951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG  
 1001 CTTGAGAAAG TCAAAGATTT TAACCTCAAC TACTATTTAA CAAAATCTTG  
 1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA AAAAAAATC GAAAACCTGA  
 1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC  
 1151 TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA  
 1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC  
 1251 AAAAGAAAGT TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTAC  
 1301 AAAAATTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA  
 1351 GGTGAGACC TCTGCAAAGC ATTTTATTA TTTTGATCAC GAAAACATCT  
 1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG  
 1451 CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA  
 1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA  
 1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT  
 1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT  
 1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG  
 1701 TAAATTCAGA CCGGAAGACT ACAAATTAAT CTACAAATAC GAAGTTATTG  
 1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TAAAGATCC  
 1801 TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG  
 1851 AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAAACT CTCTTTGCA  
 1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAATATC  
 1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA  
 2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC  
 2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT  
 2101 TGCATTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG  
 2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA  
 2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG  
 2251 CCAATATAAT TACATTAAT TTAATGGGAA GTTTTATAAA CAAACAAAAG  
 2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTATC ATTTTATTAT

FIGURE 9 (cont.)

2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA  
2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC  
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT  
2501 ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA  
2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA  
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC  
2651 TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT  
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT  
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTAATGAA TAACATTACC  
2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAACTCT  
2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG  
2901 AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC  
2951 TTAGAGGTAT CTAATAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA  
3001 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG  
3051 ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA  
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA  
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA  
3201 CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTGG TCTTATATAC  
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

FIGURE 10

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD  
51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL  
101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM  
151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA  
201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNNMKSRTTR IFYCTHFNRN  
251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIKKLK DKVIEKIAM  
301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS  
351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHელი  
401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWIFEDLVVS  
451 LIRCFYVTE QQKSYSTYY YRKNWDVIM KMSIADLKKE TLAEVQEKEV  
501 EEWKKS LGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL  
551 NSHMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA  
601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVDSKN  
651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLLIVEAKQ  
701 RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY  
751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIKEL  
801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI  
851 SIDMKTALM PNINLRIEGL CTLNLNMQT KKASMWLKKK LKSFLMNNIT  
901 HYFRKTITTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID  
951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK  
1001 KYIFNRVCM I LKAKEAKLKS DQCQSLIQYD A

FIGURE 11

1 CCCCCAAACC CCAAAACCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG  
 51 GTAGTTTAGA AATAAAATAT TATCCCGCA CAAATGGAGA TGGATATTGA  
 101 TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA  
 151 GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA  
 201 TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT  
 251 CTCGGATGCA AATCTTTATA ACGATTCTTT CTGAGAAAA TTAGTTTTAA  
 301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA  
 351 AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA  
 401 TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTT  
 451 CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG  
 501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG  
 551 AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCTG  
 601 TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC  
 651 TTGAGACAAT TGAAAAAGCT GTTTACAAC GAAGGAATCG CAGTTCTGAA  
 701 AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT  
 751 CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT  
 801 TAATGGAATA TACGTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA  
 851 TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTIAGC  
 901 TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT  
 951 AAAAGAAGCA GCGGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAT  
 1001 TTGTTGATTCTTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA  
 1051 AAAGAAGAAG AGCTATCACA ATCCTGATTCTTAAAGATTT CAAAAATTCC  
 1101 AGGTAAGAGA GATACATTCA TTAATAATTCA TATATTATAG TTTTTCATTT  
 1151 CACAGCTGTT ATTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA  
 1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT  
 1251 TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA  
 1301 GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC  
 1351 AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA  
 1401 AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG  
 1451 ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA  
 1501 GTAACTTTAA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG  
 1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA  
 1601 ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA  
 1651 AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA  
 1701 AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT  
 1751 GGGGTTTTGG GG

FIGURE 12

1 CCCCCAACCCCAAAACCCCAAAACCCCTATAAAAAAGAAAAAATTGAGGTAGTTTAGA 60  
 GGGGTTTGGGGTTTGGGGTTTGGGGATATTTTTTCTTTTAACTCCATCAAATCT  
 a P Q N P K T P K P L \* K K K K L R \* F R -  
 b P K T P K P Q N P Y K K R K N C G S L E -  
 c P K P Q N P K T P I K K E K I E V V \* K -  
 AATAAAATATTATTCGCCACAAATGGAGATGGATATTGATTGGATGATATAGAAAATT  
 61 TATTTTATAATAAGGGCGTGTACCTCTACCTATAACTAAACCTACTATATCTTTAA 120  
 a N K I L F P H K W R W I L I W M I \* K I -  
 b I K Y Y S R T N G D G Y C F G C Y R K F -  
 c \* N I I P A Q M E M D I D L D D I E N L -  
 TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA  
 121 ATGAAGGATTATGTAAGTTGTTTCATATCGTCGAGAACATCACTGTTCTTTCCTACGTTTT 180  
 a Y F L I H S T S I A A L V V T R K D A K -  
 b T S \* Y I Q Q V \* Q L L \* \* Q E R M Q N -  
 c L P N T F N K Y S S S C S D K K G C K T -  
 CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG  
 181 GTAACTTTAGACCGAGCTTTAGCGGAAGTAACGTATAAGGTTTCAACGTTTTTGTAAATC 240  
 a H C N L A R N R L H C L F Q S C K N N \* -  
 b I E I W L E I A F I D Y S K V A K T I R -  
 c L K S G S K S P S L T I P K L Q K Q L E -  
 AGTTCTACTTCTCGGATGCAAACTTTTATAACGATTCTTTCTTGAGAAAATTAGTTTAA  
 241 TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTTAATCAAATT 300  
 a S S T S R M Q I F I T I L S C E N \* F \* -  
 b V L L L G C K S L \* R F F L E K I S F K -  
 c F Y F S D A N L Y N D S F L R K L V L K -  
 AAAGCGGAGAGCAAAGAGTAGAAATGAAACATTACTAATGTTTAAATAAAATCAGGTAA  
 301 TTTCGCCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTAGTCCATT 360  
 a K A E S K E \* K L K H Y \* C L N K I R \* -  
 b K R R A K S R N C N I T N V \* I K S G N -  
 c S G E Q R V E I E T L L M F K \* N Q V M -  
 TGAGGATTATTCTATTTTATAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA  
 361 ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTAATGAATT 420  
 a C G L F Y F L D H F L R S I M E K I T \* -  
 b E D Y S I F \* I T S \* G A L W R K L L N -  
 c R I I L F F R S L L K E H Y G E N Y L I -  
 TACTAAAGGTAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT  
 421 ATGATTTTCCATTTGTCAAACCTAATAAAGGATCGGTTGTTACTACTCATATAATTAA 480  
 a Y \* K V N S L D Y F P S Q Q C C V Y \* I -  
 b T K R \* T V W I I S L A N N D E Y I K F -  
 c L K G K Q F G L F P \* P T M M S I L N S -

FIGURE 12 (cont.)

481 CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT 540  
 GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA

a H M R M S Q R I S I H Q T Y Q R Q T R Y -  
 b I C E C V K G S R Y I R L T K D K L A I -  
 c Y E N E S K D L D T S D L P K T N S L \*

541 AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTACTATTTCG 600  
 TTTTGC GTTCTTTTCAAACCTATTAGCTTGTCTGCTTCTTGAATAACGTAAATGATAAGC

a K T Q E K V C \* S N S R R T Y C I Y Y S -  
 b K R K K K F D N R T A E E L I A F T I R -  
 c N A R K S L I I E Q Q K N L L H L L F V -

601 TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACCTCCGAGTCTTGAGACAAT 660  
 ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA

a Y G F Y Y N C F R Y R R C T P E S C D N -  
 b M G F I T I V L G I D G E L P S L E T I -  
 c W V L L Q L F \* V S T V N S R V L R Q L -

661 TGAAAAAGCTGTTTACAACGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT 720  
 ACTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTCAAGACTACACATACGGTA

a C K S C L Q L K E S Q F C K F \* C V C H -  
 b E K A V Y N C R N R S S E S S D V Y A I -  
 c K K L F T T E G I A V L K V L M C M P L -

721 TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA 780  
 ATAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT

a Y F V N \* S Q I S Y L N L M D S Y R N K -  
 b I L C I N L K Y L I S I \* W I A I E T N -  
 c F C E L I S N I L S Q F N G \* L \* K Q T -

781 CCAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC 840  
 GGTTTATTTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG

a P N K P C K F N G I Y V K S F G T N A H -  
 b Q I N H A S L M E Y T L N P L G Q M H T -  
 c K \* T M Q V \* W N I R \* I L W D K C T L -

841 TGAATTTATATTGGATTCTTAAAGCATAGATACAGAAATGCTTTAGAGACTGATTAGC 900  
 ACTTAAATATAACCTAAGAATTTCTGATCTATGTGTCTTACGAAATCTCTGACTAAATCG

a C I Y I G F L K H R Y T E C F R D C F S -  
 b E F I L D S \* S I D T Q N A L E T D L A -  
 c N L Y W I L K A \* I H R M L \* R L I \* L -

901 TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA 960  
 AATGTTGCTCTAATGGACAAAACCTAATGAGAACGAGTAGAGAATATAGAAATTTCTTCGT

a L Q Q I T C F D Y S C S S L I S L K E A -  
 b Y N R L P V L I T L A H L L Y L \* K K Q -  
 c T T D Y L F C L L L L I S Y I F K R S R -

961 GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC 1020  
 CCGTTTACTTTTCTTCTGATTCTTTCTCTAAAGTTTAAACAACCTAAGAAGACATTGG

a G E M K R R L K K E I S K F V D S S V T -  
 b A K C K E D \* R K R F Q N L L I L L \* P -  
 c R N E K K T K E R D F K I C C F F C N R -

1021 GGAATTAACAACAAGAAATATTAGCAACGAAAAAGAAGAGCTATCACAATCCTGATTC 1080  
 CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTCTCGATAGTGTAGGACTAAG

a G I N N K N I S N E K E E E L S Q S C F -  
 b E L T T R I L A T K K K K S Y H N P D S -  
 c N \* Q Q E Y \* Q R K R R R A I T I L I L -

[illegible]

a  
b  
c

**FIGURE 12 (cont.)**

```

1681  GTACAGAAGTGAAGAAATAAAAGATTATTTTTCATTAATTTTATGAAAAGAGGGGT
      +-----+-----+-----+-----+-----+
      CATGCTCTTCACTTCTTTATTTTCTAAATAAAAAAAGTTATTAATAACTTTTCTCCCCAA
      1740

a  V  Q  K  C  R  N  K  R  F  I  F  F  N  N  L  L  K  R  G  V  -
b  Y  R  S  E  E  I  K  D  L  F  F  S  I  I  Y  C  K  E  G  F  -
c  T  E  V  K  K  *  K  I  Y  F  F  Q  *  F  I  E  K  R  G  F  -

      TTGGGGTTTTGGGGTTTTGGGG
1741  -----+-----  1762
      AACCCCAAAACCCCAAAACCCC

a  L  G  F  W  G  F  G  -
b  W  G  F  G  V  L  G  -
c  G  V  L  G  F  W  -

```

[illegible]







FIGURE 15

[illegible]

FIGURE 16

```

      1 MEMDIDLDDIENL....LPNTFNKYSSSCSKDKGCKTLKSGSKSPS... 42
        :|::||::||::||::||::||::||::||::||::||::||::||::||
    491 IELAIAKIIVNKNLDEIKGHTAIFSDVSGSMSTSMGGAKYGSVRTCLEC   540
        :|::||::||::||::||::||::||::||::||::||::||::||::||
      43 .LTIPKLQKO.....LEFYFDANLYNDSFRLKLVLSKGQRVEIETLL   85
        :|::||::||::||::||::||::||::||::||::||::||::||::||
    541 ALVLGLMVQRCEKSSFYIFSSPSSQCNCXYL.EVDLPGEDELPSMQKLL   589

```

[illegible]

FIGURE 17

	Motif A	Motif B
Consensus	h--h <h>h</h> ---h--h	h---- <h>h</h> --- <h>h</h>
telomerase p123	QPKLFFATMDIEKCYDSVNREKLSFLKTKLL-100-RFYKQTKGIP <h>h</h> LCVSSILSSFFYYATLEESSLGF	QPKLFFATMDIEKCYDSVNREKLSFLKTKLL-100-RFYKQTKGIP <h>h</h> LCVSSILSSFFYYATLEESSLGF
Dong (LINE)	KNRNHLHCTYIDYKAFDSIPHSWLIQVLEIYKIN-28-RQIAIKGIY <h>h</h> DSLSPLWFCLALNPLSHQLHNR	KNRNHLHCTYIDYKAFDSIPHSWLIQVLEIYKIN-28-RQIAIKGIY <h>h</h> DSLSPLWFCLALNPLSHQLHNR
a1 S.c. (group II)	FGGSNWFFREVDLKKCFDTISHDLIIKELKRYISD-26-HVPVGRVCV <h>h</h> APTSALCNVALLRLDRRLAGLA	FGGSNWFFREVDLKKCFDTISHDLIIKELKRYISD-26-HVPVGRVCV <h>h</h> APTSALCNVALLRLDRRLAGLA
HIV-RT	LKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP-7-GIRYQYNVLP <h>h</h> WKGSPIAFQSSMTKILEPFRKQN	LKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP-7-GIRYQYNVLP <h>h</h> WKGSPIAFQSSMTKILEPFRKQN
L8543.12	VLPELYFMKE <h>h</h> VKSCYDSIPRMECMRILKDALKN-68-KCYIREDEGLF <h>h</h> ESSLSA?IVDLVYDDLLLEFYSEPK	VLPELYFMKE <h>h</h> VKSCYDSIPRMECMRILKDALKN-68-KCYIREDEGLF <h>h</h> ESSLSA?IVDLVYDDLLLEFYSEPK

	Motif C	Motif D	Motif E
Consensus	h--Y <h>h</h> DD <h>h</h> hh	<h>h</h> -h-- <h>h</h> - <h>h</h>	h-h <h>h</h> -h
telomerase p123	-14-LMRLLTDDYLLITTOENN-0-AVLFIKLINVSRENG <h>h</h> KYMERKLT-23-QDYCDWIGISI	<h>h</h> -h-- <h>h</h> - <h>h</h>	h-h <h>h</h> -h
Dong (LINE)	-16-HLIYMDDIKLYAKNDKE-0-MKKLIDTTTIFSNDISMQFGLDKCKT-25-KC-YKYLGFQQ	<h>h</h> -h-- <h>h</h> - <h>h</h>	h-h <h>h</h> -h
a1 S.c. (group II)	-55-YVRYADDLIGVLGSKN-2-KIKRDLNFLNS.IGLTINEERTLI-4-ET?ARFLGYNI	<h>h</h> -h-- <h>h</h> - <h>h</h>	h-h <h>h</h> -h
HIV-RT	-4-IYQYMDLIVGSHLEIG-1-HRTKTEELRQHLRLWGLTTPDKHQK-0-EP?FLWMGYEL	<h>h</h> -h-- <h>h</h> - <h>h</h>	h-h <h>h</h> -h
L8543.12	-8-ILKLADDFLIISTDQQ.....VINIKKLAMCG <h>h</h> QKYNARANR-41-IRSKSSKGIFR	<h>h</h> -h-- <h>h</h> - <h>h</h>	h-h <h>h</h> -h

FIGURE 18

telomerase p43	LQKQIEFYSDANLYNDSFLRKLVLSGEQRVEIETLLM
human La	ICHQIEFYEGDFNLPRDKFLKEQI.KLDEGWVPLEIMIK
Xenopus LaA	ICEQIEFYEGDFNLPRDKFLKQOI.LLDDGWVPLETMIK
Drosophila La	ILROVEFYEGDANLNRDKFLREQIGKNEDGWVPLSVLVT
S. c. Lhplp	CLKQVEFYSEFNFPYDFELRTTAEK.NDGWVPISTIAT

FIGURE 19

1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa  
 61 tagatttaatt ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata  
 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga  
 181 tatataagtt agggttaaga ttgacgatcc taagcaatat ctggtgaacg tcaactgcagc  
 241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac  
 301 taaagcactt ctgaggtgg ctgagttga tctgagttc atctgctagt tggcagttc  
 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgtgt  
 421 ccacaagaat actcaacat tcatgaaaa gtacttcaac aaagcagtac tttgcctaa  
 481 tgacttactg gaagtctgtg aatttgata ggttctctat attttgatg caactgaatt  
 541 caaaaatttg tatcttgata ggatacttc ataagatatt cgttaaggaaac tcaacttccg  
 601 taagtgttta caaagatgcg tcagaagcaa gtttctgaa ttcaacgaat actaacttgg  
 661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa  
 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta  
 781 ggcaataaag gaatctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga  
 841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc  
 901 catgaagaaa cacatgaagg cacctaaaat tcttaactct accttggaaat caaagtactt  
 961 gaccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa  
 1021 gatccttggg aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgattc  
 1081 tgcacttgca ccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa  
 1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaatt  
 1201 ttcaagcaat taactccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc  
 1261 cgggttttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt  
 1321 tgagaactcc aagatgttcc ctcttcaatt cttagtgcc attgaagctg ttaatgaagc  
 1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaaag gtcaaatcga  
 1441 agcagtaaaag gaagtgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta  
 1501 aaccgaagaa ggagaatttg ttaaagtcaa cgaaggaatt ggcaagcaat acattaactc  
 1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca aaggacacac  
 1621 tgcaatcttc tctgatgtt ctggttctat gactacctca atgtcaggtg gagccaagaa  
 1681 gtatggttcc gttcgtactt gtctcgagtg tgcattagtc ctgtgttga tggtaaaata  
 1741 acgttgtgaa aagtctcat tctacatctt cagttcacct agttctcaat gcaataagtg  
 1801 ttacttagaa gttgatctcc ctggagacga actccgtcct tctatgtaaa aacttttgca  
 1861 agagaaaagga aaacttgggtg gtgttactga ttcccctat gattgcatg atgaatggac  
 1921 aaagaataaa actcacgtag acaatatcgt tatttgtct gatatgatga ttgcagaagg  
 1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga  
 2041 tgaagtaaat cctaacatta aaactttgc agttgactta gaaggttacg gaaagtgcct  
 2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggtg tgagcgattc  
 2161 aatcttaaag ttcatctcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa  
 2221 cttgcccct caaaaaatag gacaaaagtg agtttctga gattcttcta taacaaaaat  
 2281 ctacccccac tttttgtt tattgcatag ccattatgaa atttaatta ttatctattt  
 2341 atttaagtta cttacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc  
 2401 aaagaacaaa aaagattaaa a

## FIGURE 20

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL  
VNVTAACLLQEGSYQDKDERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTTN  
YIVAFVCVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS  
QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMTFRYLSVTNKQKWDQTK  
KKRKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKIAKRQNAMKKHMK  
APKIPNSTLESKYLTFFKDLIKFCHISEPKERVYKILGKKYPKTEEEYKAAFSDSASAP  
FNPELAGKRMKIEISK TWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGV  
SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNKGGQIE  
AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKIAVNKNLDEIKG  
HTAIFSDVSGSMSTMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ  
CNKCYLEVLDLPGDEL RPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHTVDNIVILSD  
MMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFAVDLEGY GKCLNLGDEFNENNYI  
KIFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK



# FIGURE 21

1 tcaatactat taattaataa ataaaaaaaaa gcaaaactaca aagaaaatgt caaggcgtaa  
 61 ctaaaaaaag ccataggctc ctataggcaa tgaacaaat ctgtatttg tattacaaaa  
 121 tctagaagt tacaaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga  
 181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga  
 241 tgatgatgat gaagaaaaca actcaataa ataataagaa ttattaagga gagtcaatta  
 301 gattaagtag caagttaat tgataaaaa agttgggtct aaggtagaga aagatttgaa  
 361 ttgaacgaa gatgaaaaa aaaagaatgg actttctgaa tagcaagtga aagaagagta  
 421 attagaacg attactgaag aatagggtta gtattaaat ttagtattia acatggacta  
 481 ccagttagat ttaaatgaga gtgggtggcca tagaagacac agaagagaaa cagattatga  
 541 tactgaaaaa tggttgaaa tatctcatga ccaaaaaaat tatgtatcaa ttacggcaa  
 601 ctaaaagaca tcatattgtt ggtggcctaa agattatttt aataaaaaa attatgatca  
 661 tcttaagtga agcattaaca gactagaac tgaagccgaa ttctatgcct ttgatgatt  
 721 ttcaaaaca atcaaaacta ctaataattc ttactagact gttacatag acgttaatt  
 781 tgataaat ctctgtatc tcgcattgct tagattttta ttactactag aaagattcaa  
 841 tattttgaat ataagatctt ctatacaag aaattaatat aattttgaga aaattggtga  
 901 gctactgaa actatcttcg cagttgtctt ttctatcgc cacttacaag gcattcatt  
 961 acaagtctt tgggaagcgt tctaatttt agttaactcc tcatcataaa ttacggttaa  
 1021 agatagctaa ttataggat actctttctc tacagactta aaattagttg acactaaca  
 1081 agtccaagat tattttaagt tctataaga attccctcgt ttgactcatg taagctagta  
 1141 ggctatccca gtagtgcta ctaacgctgt agagaacctc aatgtttac ttaaaaagg  
 1201 caagcatgct aatcttaatt tagtttctat cctaccta tcaattttg atttctact  
 1261 tgttaattta taacatttga aattagagti tggattagaa ccaaatattt tgacaaaaca  
 1321 aaagcttgaa aatctacttt tgagtataaa ataatacaaa aatcttaaat tttaagatt  
 1381 aaactttac acctacgttg ctaagaacac ctccagaaaa cagatattaa aacaagctac  
 1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaaagatga  
 1501 aactccaagc gaaagcaca gtggtatgaa atttttgat catctttctg aattaaccga  
 1561 gcttgaagat ttacagcgtta acttgaagc tacccaagaa atttatgata gcttgcaca  
 1621 acttttgatt agatcaaca atttaagaa gttcaatta agttacaaat atgaaatgga  
 1681 aaagagtaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct  
 1741 taaagatgc tctgttaata tatcaaatcc tcatggaac atttcttatg aactgacaaa  
 1801 taaagattct acttttata aatttaagct gacctaaac taagaattat aacacgctaa  
 1861 gtatactttt aagtagaacg aattttaatt taataacgtt aaaagtgc aaattgaatc  
 1921 ttctcatta gaaagcttag aagatattga tagtctttgc aaatctattg ctcttgtaa  
 1981 aaatttaca aatgttaata ttatcgccag ttgctctat cccaacaata tttagaaaa  
 2041 tctttcaat aagcccaatc ttctatttt caagcaattt gaataattga aaaatttga  
 2101 aaatgtatct atcaactgta ttcttgatca gcataactt aattctattt cagaattctt  
 2161 agaaaagaat aaaaaataa aagcattcat ttgaaaaga tattatttat tacaatatta  
 2221 tcttgattat actaaattat taaaacact tcaatagta cctgaattaa attagttta  
 2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaa  
 2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaagaat catcctaac  
 2401 ccttagcta atagattttg accaaaacac tgtaagtgtat gactctatta aaaagatttt  
 2461 agaacttata tctgagtcta agtatcatca ttatttgaga ttgaacctt gttaatctag  
 2521 cagtttaatt aaatctgaaa acgaagaat ttaagaactt ctcaagctt gcgacgaaa  
 2581 aggtgtttta gtaaaagcat actataaatt ccctctatgt ttaccaactg gtacttatta  
 2641 cgattacaat tcagatagat ggtgattaat taaatattag tttaataaaa tattaatat  
 2701 tgaatatttc ttgcttatt attgaataa tacatacaat agtcattttt agtgtttga  
 2761 atatatttta gttattaat tcattatttt aagtaataa ttattttca atcattttt  
 2821 aaaaaatcg

## FIGURE 22

MSRRNQKKPQAPIGNETNLDVFLQNLEVYKSQIEHYKTQQQIK  
EEDLKLLKFKNQDQDGNSGNDDDEENNSNKQQELLRRVNQIKQQVQLIKKVGSKVEK  
DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR  
ETDYDTEKWEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNDHLNVSINRLETEAE  
FYAFDDFSQTIKLTNNSYQTVNIDVNFNNLCILALLRFLSLERFNILNIRSSYTRN  
QYNFEKIGELLETIFAVVFSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF  
STDCLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL  
VSIPTQFNFDYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNLKFLRLNFYTY  
VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED  
FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLK  
RCSVNISNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSAKIE  
SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNLLFFKQFEQLK  
NLENSINCILDQHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKLFKTLQQLPE  
LNQVYINQQLLELTVSEVHKQVWENHKQKAFYEPLCEFIKESSTLQLIDFDQNTVSD  
DSIKKILESISESKYHHYLRNPSQSSSLIKSENEEQELLKACDEKGVLVKAYYKFP  
LCLPTGTYYDYNSDRW

### FIGURE 23

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL  
PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKIARNEDVNNSLFCBS  
ANVNVTLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK  
WVQRSSSSSATAAQIKQLTEPVTNKQFLHKLNNSSSFFPYSKILPSSSSIKKLTDLR  
EAIPTNLVKIPQRLKVRINLTQKLLKRHKRLNYVSILNSICPPLEGTVLDLSHLR  
QSPKERVLFHIVILQKLLPQEMFGSKKNKGKIIKNLNLSSLPNGYLPFDSLLKKL  
RLKDFRWLFISDIWFTKHNFNENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVTI  
VYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLNHNHSMRIIPKKSNNFR  
IIAIPCRGADEEEFTTYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE  
FKQRLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN  
TNTGVLKLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY  
IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV  
INIKKLAMGGFQKYNANRDKILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN  
NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNLSTNTVLMQIDHVVKNISECYKSAF  
KDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIEYEVRFITLNGFLESLSNTS  
KFKDNIILLRKEIQHLQAYIYIYIHIVN

FIGURE 23

# FIGURE 24

*Oxytricha*  
*Euplotes*

LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT  
LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIGURE 25

Motif 0

human	AKFLHWLMSVYVVELLRSPFYVTETTFQKNR
tez1	ISEIEWLVLGKRSNAKMCLSDFEKRKQIFAEFIYWLNSPIIPILQSFFYITESSDLNR
EST2	LKDFRWLFISD---IWFTKHNFENLNQLAICFISWLPRLPKIIQTFFYCTEISSTVT-
p123	TREISWMQVET-SAKHFIYFDHEN-IYVLWKLRLWIFEDLVVSLIRCFYVTEQQKSYK

. \* . . . . \* \* \*

Motif 1

human	LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALTSRLRFIPKP--DGL
tez1	TVYFRKDIWKLLCRPFI-TSMKMEAFKINENNVRMDTQK-TTLPPAVIRLLPKK--MTF
EST2	IVYFRHDTWNKLITPFIVEYFKTYLVENMVCRNHSYTLS--NFNHSMRIIPKKSNEF
p123	TYYYRKNIWDVIMKMSI-ADLKKETLAEVQEKEVEEWKKS-LGFAPGKLRLLPKK--TTF

. . . \* . \* \* . . . \* \* \*

Motif 2

human	RPVNM DYVVGARTFRREKRAERLTSRVKALF-SVLNYERA
tez1	RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLNEESSGIPFNLEVYMKLLTF
EST2	RIIAIPCRGADEEEFTIYKENHKMAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF
p123	RPIMTFNKKIVNSDRKTTKLTNTNKLKLNHMLKTLKN-RMFKDPPGFAVFNYDDVMKKY

\* \* . \* . \* . . .

Motif 3 (A)

tez1	KKDLLKHRMFGR-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEFVIRKYATIHATS
EST2	KQRLKKKFNNVLPelyfMkFDVKSyDSIPMECMRILKD-ALKNENGFFVRSQYFPNTN
p123	EEFVCKWKQVGQPKLPFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKN

. \* . \* \* . . . \* \*

FIGURE 26

ATTTATACTCATGAAAATCTTATTTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA  
 GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT  
 TCTAACTACGTGTTTCGCACTACCAAATTCAAGAAAAATAGCATTACCATGCCTTCCTGG  
 TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT  
 ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG  
 TCTTTTTTGGCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGGAAAAT  
 GTTCCACAGTTTGGTCCGTACATACGCATTGCTTGATTTATTGATCAATTATACAGTAAT  
 TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAAACAGATGTAACGAACCTCATCT  
 GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA  
 ACTTACAGAACCAGTGACAAATAACAATTCTTACACAAGCTCAATATAAAATTCCTCTTC  
 TTTTTTTCCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT  
 GAGAGAAGCTATTTTTCCCAAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT  
 TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT  
 GAATAGTATTTGCCACCATTGGAAGGGACCGTATTGGACTTGTGCGATTGTGAGTAGGCA  
 ATCACCAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAGTTATTACCCCA  
 AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTATCAAGAATCTAAATCTTTTATT  
 AAGTTTACCCTTAAATGGCTATTTACCATTGATAGTTTGTGAAAAAGTTAAGATTAAA  
 GGATTTTCGGTGGTTGTTTCAATTTCTGATATTTGGTTCACCAAGCACAAATTTGAAAACCTT  
 GAATCAATTGGCGATTTGTTTCAATTTCTGGCTATTTAGACAATAATTCCCAAAATTAT  
 ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA  
 TGATACTTGGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTACTTAGT  
 CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA  
 AATGAGGATTATACCAAAAAAAGTAATAATGAGTTCAGGATTATTGCCATCCCATGCAG  
 AGGGGCAGACGAAGAAGAAATTCACAATTTATAAGGAGAATCACAAAATGCTATCCAGCC  
 CACTCAAAAATTTTAGAATAACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA  
 TTCTCCAACGCAAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAATT  
 TAATAATGTCTTACCAGAGCTTTATTTTCATGAAATTTGATGTCAAATCTTGCTATGATTC  
 CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGT  
 TTTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT  
 TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT  
 TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAACAGCTTT  
 GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTTCAGGGCTCTAGTTTATC  
 TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC  
 CAGTCTTAGCCAGGACACATTAATTTTAAAACCTGGCTGACGATTTCTTATAATATCAAC  
 AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA  
 TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT  
 TATTCATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAAACATTCAAG  
 CACAATGAATAATTTCCATATCCGTTGAAATCTAGTAAAGGGATATTTGGAAGTTTAAAT  
 AGCGCTGTTTAAACACTAGAATCTCTTATAAAACAATTGACACAAAATTTAAATTCAACAAA  
 CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTGGAATGTTATAAATCTGC  
 TTTTAAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTCAATCGTTCTTACAACG  
 CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA  
 TGAGGTACGATTCACCATATTGAATGGATTTTTGGAAGCCTATCTTCAAACACATCAAA  
 ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCAACACTTGCAAGC

09756353 014001

FIGURE 27

AKFLHWLMSVYVVELLSFFYVTETTFQKNRLFFYRKS VWSKLQSIGIRQHLKR  
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPVNM DYVVGARTFRREKR  
AERLTSRVKALFSVLNYERA

FIGURE 28

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC  
TTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACC  
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAA  
GAGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGA  
AGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACG  
GGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCG  
CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGC  
GTGCTCAACTACGAGCGGGCGCG



FIGURE 29

MTEHHTPKSRILRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF  
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHEDFRAMHVNGVQNDLV  
STFPNYLISILESKNWQLLLEIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRK  
RTIETSITQNK SARKEVSWNSISISRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMWLQWIFPRQFG  
LINAQVVKQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS  
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEIEWLVL  
GKR SNAKMCLSDFEKRKQIFAEFIYWL YNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFIT  
SMKMEAFEKINENNVRMDTQKTTLPPAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTNQT  
LRPVASILKHLIN EESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLMFR  
IVKKKLDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKV VQLLSMKTSDTLFVDFVDY  
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL  
LRVVDDFLFITVNKKDAKKFLNLSLRGF EKHNFSTSEKTVIN FENSNGIINNTFFNESKKRMPFFG  
FSVNMRLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCNI  
YRLGYSMCMRAQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFC  
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLFHRRAD

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FIGURE 30

ggtagcgattactttcttctcataagctaattgcttctcgaacgctcctaatactctggaaatattttacaagaactcaataacaataccaagtc aaattccaatatgaagg  
 tgttattagtgatcgataaatttctattttatcggtcgttaccagataaggacaaaagaacaacttctccccctaaagacttttactttatattactttcaaatatattcg  
 ggttcgcttacttttaacgttggtactgttttagctgctacttctagccaaccgctgtttctaccccgctcattggatagctcttggagtagctcacagaaatccttcaaatctt  
 ctgatgagactatattagattcattacagtcggtcgcataattcttaacatggagccttacactttagatgagtcacgctgcgatggagtagtttggatcatccaacggttgccttg  
 aaaagggtgataaattattgcaaaatcatgctccttagtggtggaatccgcgaaagtgtttgatgcttcacacgcttagcatgattgagatattcaaaatttctatccactacaa  
 ctctttaaaccggttttattttctatttctcatgttggtccaatatgtatcatctcgtattaggctttttccggtttactcctggaatcgtaaccttttactattccccctaatg  
 aataatctaaattagtttcgcttataattgatagtagtagaagattggtgattctactcgtgtaattgtattagtttaaagatactttgcaaaacatttattagctatcattatataaaa  
 aaaatcctataattataaataattatcaatttgcggtcactatttattaaaacggtatgatcagtaggacactttgcatatatatagttatgcttaattggttacttgaacttgcAT  
 GACCGAACACCATACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTA  
 CCTTAAATGATTATGTACAACCTTGTGAGAGGGTTCGCCGGAAGCTCGTATAGCAATATATGCGAA  
 CGCTTGAGAAGCGATGTACAAACGTCCTTTTCTATTTTCTTCATTTCGACTGTAGTCGGCTTCGACAGT  
 AAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAAATGCTCACAGTCAGAGgtatatataattttgtttgattttttctattcg  
 ggatagctaataatagggcagCTAATAGCGAATGTTGTAAAACAGATGTTTCGATGAAAGTTTGTAGCGTCGAAGGA  
 ATCTACTGATGAAAGGGTTTCCATGgttaaggatttctaattgtgaatatttacctgcaattactgttcaagagattgtatttaaccgataaagAA  
 TCATGAAGATTTTCGAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCCTAATTA  
 CCTTATATCTATAGTCTGAGTCAAAAAAATTGGCAACTTTTGTAGAAAATgttaataaccggttaagattgttgcgcactttgaaca  
 agactgacaagtatagTATCGGCAGTGATGCCATTGCATTACTTATTATCCAAAGGAAGTATTTTGTAGGCTCTTC  
 CAAATGACAATTACCTTCAGATTTCTGGCATAACCACTTTTAAAAAATAATGTGTTTGTAGGAACTGTGT  
 CAAAAAAGAAAGCGAACCATTGAAACATCCATTACTCAAAAATAAAGCGCCCGCAAAGAAGTTTC  
 CTGGAATAGCATTCAATTAGTAGGTTTAGCATTTTACAGGTATCCTATAAGAAGTTTAAGCAAGgt  
 aactaatactgttatccttcataactaatttttagATCTATATTTTAACTTACACTCTATTTGTGATCGGAACACAGTACACATG  
 TGGCTTCAATGGATTTTCCAAAGGCAATTTGGACTTATAAACGCATTTCAGTGAAGCAATTGCACAA  
 AGTGATTCCACTGGTATCACAGAGTACAGTTGTGCCAAACGTCCTAAAGGTATACCCTTTAATTGA  
 ACAACAGCAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTATTGCCCATATATTGA  
 CACCCACGATGATGAAAAAATCCTTAGTTATTCCTTAAAGCCGAACCAGGTGTTTGCCTTCTTCGATC  
 CATTCTTGTTTCGAGTGTTTCCTAAATTAATCTGGGGTAACCAAAGGATATTTGAGATAATATTAAGg  
 tattgtataaaatttattaccactaacgattttaccagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTAC  
 ATTATTTAATGAGTAACATAAAAGtaatatgccaattttttaccattaattaacaatcagATTTTCAGAAATTGAATGGCTAGT  
 CCTTGAAAAAGGTCAAAATGCGAAAAATGTGCTTAAGTGATTTTGTAGAAACGCAAGCAAAATATTTGCGG  
 AATTCATCTACTGGCTATACAATTCGTTTATAATACCTATTTTACAATCTTTTTTATATCACTGAATC  
 AAGTGATTTACGAAATCGAACTGTTTATTTTAAAAAGATATTTGGAACTCTTGCGCCAGCCCTTTAT  
 TACATCAATGAAAAATGGAACGCTTTGAAAAATAAACGAGTatttttaagatttttgcataaattttcagAACAA  
 TGTTAGGATGGATACTCAGAAAACACTATTTGCTCCAGCAGTATTTCGTCTATTACCTAAGAAGAATAC  
 CTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAAGgtattatttttggtcatcaatgtactttacttctaattctattattag  
 cagATGGGTTCAAACAAAAAATGTTAGTCAGTACGAACCAAACTTTACGACCTGTGGCATCGATACTG  
 AAACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTAACTTGGAGGTTTACATGAAGCTTCTTACT  
 TTTAAGAAGGATCTTCTTAAGCACCGAATGTTTGGtaattatataatgcccattcctcattataattttgcagGCGTAAGAAG  
 TATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATTGTT  
 AAAAAGAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATACATGCAACAAGTGACCG  
 AGCTACAAAAAATCTTGTAGTGAGGCGTTTCTCTATTgttaagttatttttcattggaatttttaacaaattccttttagTTGATAT  
 GGTGCCTTTTGA AAAAGTCGTGCAGTTACTTTCTATGAAAACATCAGATACTTTGTTTGTGATTTTGT  
 GGATTATTGGACCAAAAGTTCTTCTGAAATTTTAAAAATGCTCAAGGAACATCTCTCTGGACACATTGT  
 TAAGgtataccaattgttgaattgtaataacactaatgaaactagATAGGAAATTCTCAATACCTTCAAAAAGTTGGTATCCCTC  
 AGGGCTCAATTCTGTCTCTTTTGTGTCTATTTCTATATGGAAGATTTGATTGATGAATACCTATCGTT  
 TACGAAAAAGAAAGGATCAGTGTTGTTACGAGTAGTCGACGATTTCTCTTTATAACAGTTAATAAAAA  
 AGGATGCAAAAAAATTTTGAATTTATCTTTAAGAGgtgagttgctgtcattcctaagttctaaccgttgaagGATTGAGAA  
 ACACAATTTTCTACGAGCCTGGAGAAAACAGTAATAAACTTTGAAAAATAGTAATGGGATAATAAACA  
 ATACTTTTTTAAATGAAAGCAAGAAAAGAAATGCCATTCTTCGTTTCTGTGAACATGAGGTCCTTTG  
 ATACATTGTTAGCATGTCTTAAATTTGATGAAGCCTTATTTAACTCTACATCTGTAGAGCTGACGAAAC  
 ATATGGGGAAATCTTTTTTACAAAAATTCTAAGgtatactgtgtaactgaataatagctgacaaataatcagATCGAGCCTTGC  
 ATCCTTTGACAAAGTATTTTATGACATTACCCACAATTCAAAATTCATTCTTGCTGCAATATATATAG  
 GCTAGGATACCTATGTGTATGAGAGCAAGCATACTTAAAAAGGATGAAGGATATATTTATTTCCCC  
 AAAGAATGTTCTATAACGGgtgagtacttattttaactagaaaagtcattaattaaccttagATCTTTTGAATGTTATTGGAAGAAAA  
 ATTTGAAAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTGTCTCTGCAGAAGTCAA

**FIGURE 30 (cont.)**

ATGgtacgtgtcgggtctcgagacttcagcaaatattgacacatcagGCTTTTTTGTCTTGGAATGAGAGATGGTTTTGAAACCTCTTT  
TCAAAATATCATCCATGCTTCGAACAGCTAATATACCAATTTTCAGTCATTGACTGATCTTATCAAGCCGC  
TAAGACCAGTTTTGCGACAGGTGTTATTTTTACATAGAAGAATAGCTGATTAAgtcattttcaatttattatatacatcctt  
tattactggtgtcttaaacaaatattattactaagtatagctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatcctgtattagtttgattgacttgcctt  
atccttatacttttaagaaagattgacagtggtgctgactactgcccacatgccattaaacgggagtggttaaacattaaaagtaatacatgaggcctaactccttcatttag  
aataaggaaagtgttttctataatgaataatgccgcactaatgcaaaaagcgaagattatctttaaacaagggggattaagcatatccgaaggaagagagtaatat  
accagtggtgtgaagaagaagcaaggataatttgaacaagcttctgcagatgacaggctaaatttggtagccgaatttggtaaagccccagggtatccatgttggtccg  
gccttgactctgagacgaaaagaaactaaggatagtttgaataactaatagctcatttaattgtcttataataagctgttttcttctgacttcaatttgcattggtgaaagaaata  
gtgttaagccattattggtatccgaaatgacaaatttctgtctcctcaagcgggaagtctaaagaacttgaagctatgatggctcctcaaaactcctctgatttaaggag  
gaatctccaccgatgaggaatgtgatgctctctagctctgtgagggaagccttaatttttcaaaaaagaaataatcatcttggagacatctcttgatgaatcagatcgga  
gagtatctccagcggatccttgatgctcaataactctatttctgaattgtatgtctactgtcgttcgacttctcgtagctctacgcagttaagtaccgaaaggtagc

FIGURE 31

EST2 pep	FFYCTEISST	VIVYFRHDT	WN----	KLIT	P-----	FIVE	YFK-TYLVEN	40
Euplotes pep	FFYVTEQOKS	YSKTYYYRKN	IWDVI-MKMS	IAD----	LKK	ETLA--EVQE		43
Trans of tetrahymen	-----KHKE	GSQIFYRKP	IWKLVSKLTI	VKVRIQFSEK	NKQMKNFYQ			44
Consensus	FFY..TE..K.	.S...YYRK.	IW...-KL..	....-F..K	.....V..			50
EST2 pep	NVCRNHNSY-	-----	TLSNFNHSKM	RIITEKSNNE	FRITAIPCRG			79
Euplotes pep	KEVEEWKKS	-----	---GFAPGKL	RIIPKMIT--	FRFIMTFNKK			78
Trans of tetrahymen	KIQLEENLE	KVEEKLIPED	SFQKYPOCKL	RIIEPKGS--	FRFIMTFLRK			92
Consensus	K...E.....	-----	....F...GKL	RIITPKI...	FRFIMTF..RK			100
EST2 pep	ADEEEFTIYK	ENHKNAIQPT	QKILEYLRNK	RPTSFTKIYS	PTQIADRIKE			129
Euplotes pep	IVNSDRKTTK	LTNTIKLLNS	RLMLKTLKN-	-----RMFK	-DPFGFAVFN			120
Trans of tetrahymen	DKQKNIK---	LNLNQILMDS	QLVFRNLKD-	-----ML-G	-QKIGYSVFD			130
Consensus	.....K..K	LN.N..L..S	QL.L..LKN-	-----	...IG..VF			150
EST2 pep	FKQRLLRNEN	NVL-----	---EELFMKFD	VKSCYD				157
Euplotes pep	YD-DVMKRYE	EFVCKWKQVG	QPKLFFATMD	IEKCYD				155
Trans of tetrahymen	NK-QISEKFA	QFIEKWKNKG	RFOLYYVTL-	-----				158
Consensus	.K-...KEF.	.F..KWK..G	.E..LYF.T.D	...CYD				186

EST2 pep  
Euplotes pep  
Trans of tetrahymen  
Consensus

FIGURE 32

S-1: FFY VTE TTF QKN RLF FYR KSV WSK  
S-2: RQH LKR VQL RDV SEA EVR QHR EA  
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q  
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS  
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV



**FIGURE 34**

Poly 4

5'- <sup>t</sup>cag <sup>a</sup>acc <sup>a</sup>aaa <sup>g</sup>gga <sup>c</sup>att <sup>c</sup>cca <sup>t</sup>taa <sup>c</sup>gg -3'  
Q T K G I P Q G

**4. (B')**

**5 (c')**

D     D     Y     L     L     I     T  
 3'- ctg ctg atg gag gag tag tgg -5'  
       a     a     a     a     a     a     a  
                       t     t     t     t  
                               c     c  
                                   Poly 1

Poly 1

[illegible]

FIGURE 35

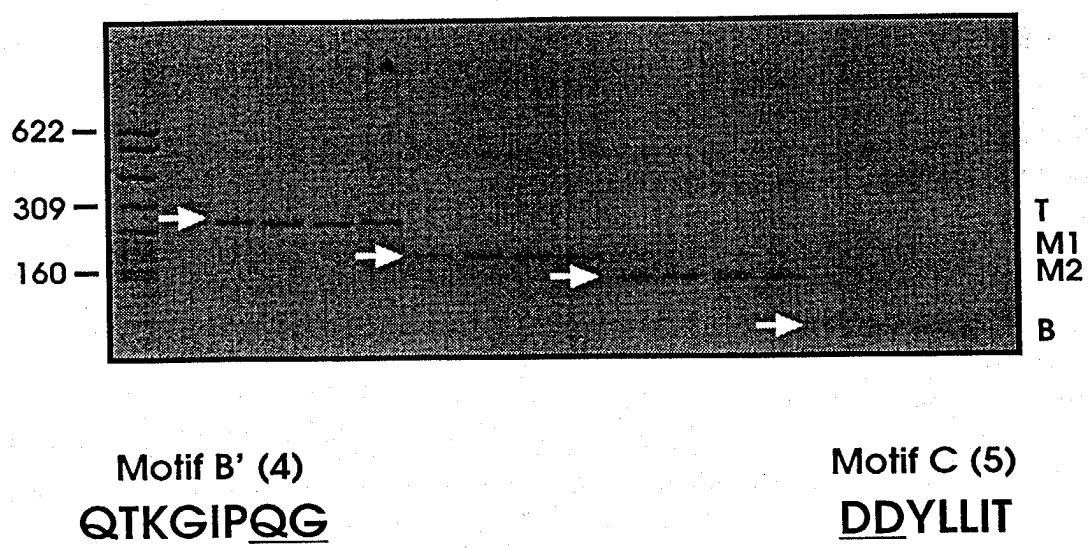




FIGURE 36

## PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

Ot	LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123	KGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2	SILSSFLCHFYMEDLIDEYLSFTKKK-----GSVLLRVV
Sc_p103	DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS

\* . \* . \* . . . . .

Q K V G I P Q G  
caa aaa gtt ggt atc cct cag gg..... <---Actual Genomic Sequence.

### Poly 4

t t c  
a a g c c t c g  
cag acc aaa gga att cca taa gg ---->

ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG  
tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

K G I P S G S I L S S F L C H F Y M

GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA  
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E D L I D E Y L S F T K K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc  
CAT CAG ctg ctg atg gag gag tag tgg

V V D D Y L L I T

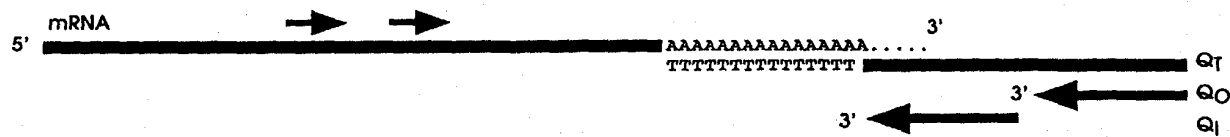
<---- ctg ctg atg gag gag tag tgg  
a a a a a a a a  
t t t t  
c c

### Poly 1

.....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence.  
D D F L F I T

FIGURE 37

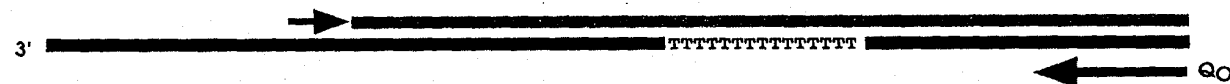
# 3' RT PCR Strategy



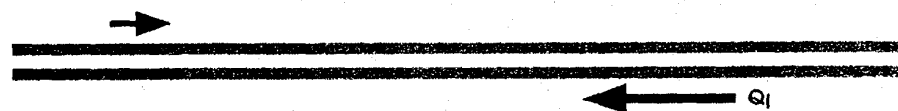
1. Synthesis of cDNA with Q<sub>T</sub> Primer.



2. First Round PCR Using Outside Primer and Q<sub>O</sub> Primer.



3. Second Round PCR Using Inside Primer and Q<sub>I</sub> Primer.



4. Sequence Second Round PCR Products Using Inside Primer or Q<sub>I</sub> Primer.

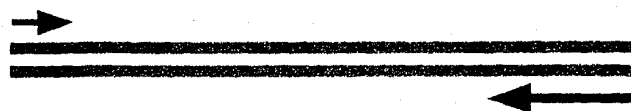


FIGURE 38

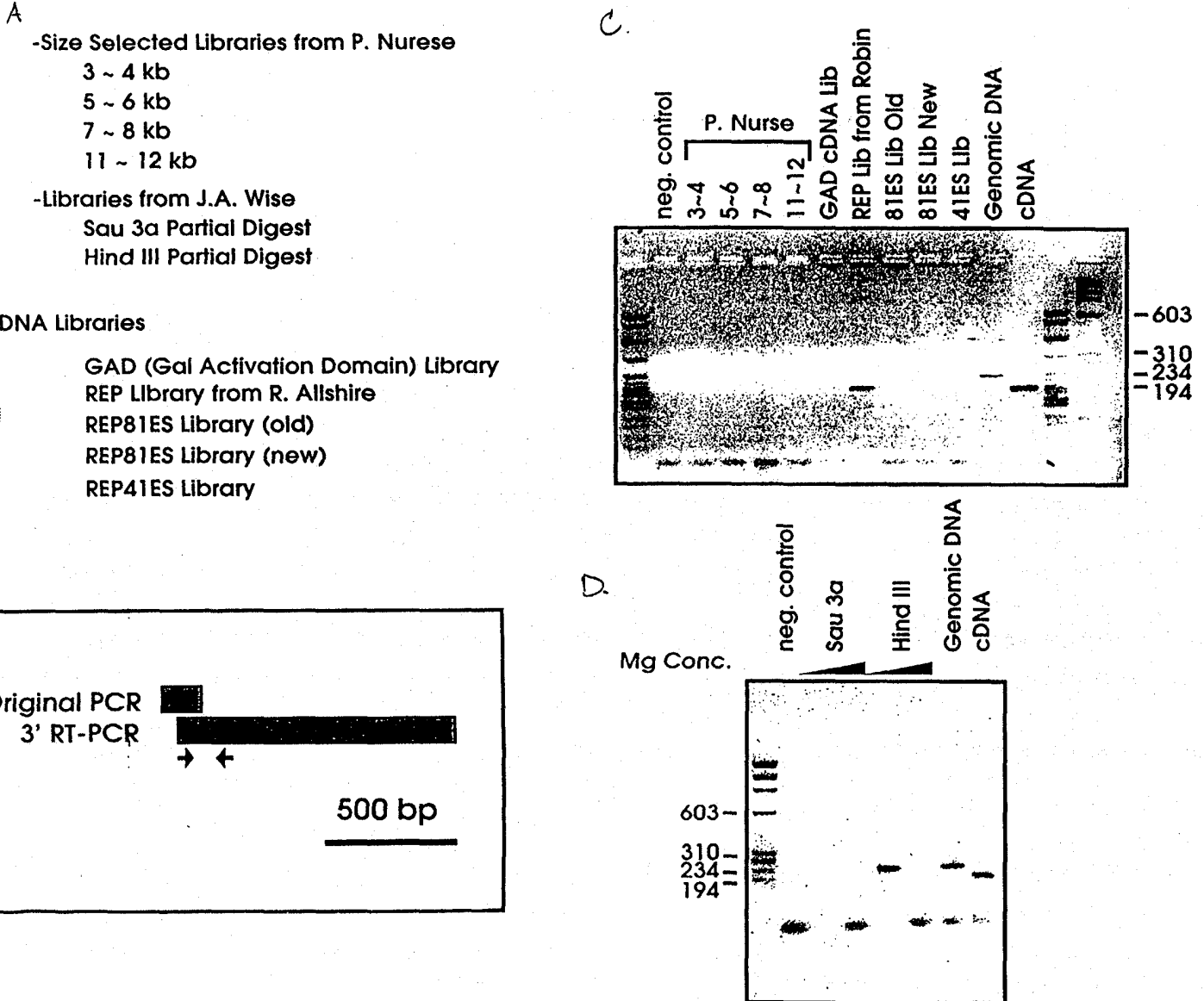
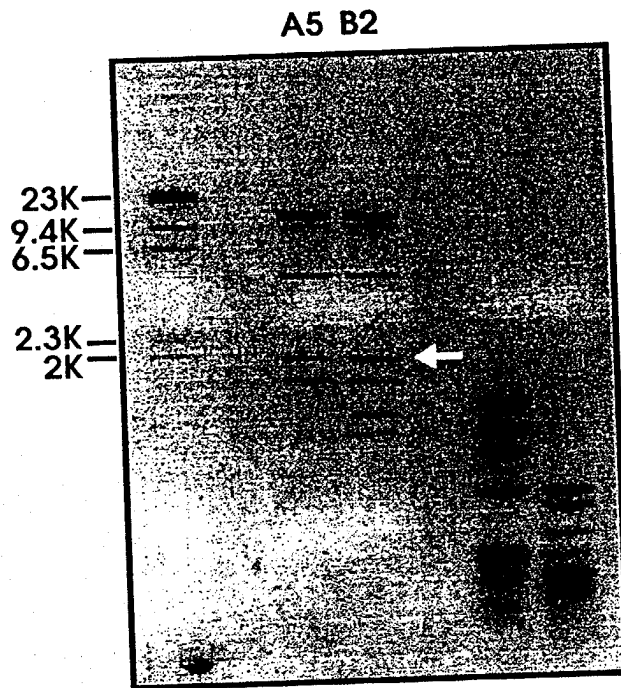


FIGURE 39



Hind III Digested Positive Genomic Clones

FIGURE 40



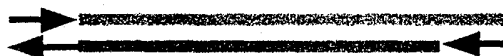
1. Synthesis of cDNA with Specific Downstream Primer.



2. Ligate Oligo with 5'-P and blocked 3' to cDNA using T4 RNA Ligase.



3. First Round PCR



4. Second Round PCR

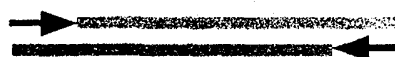


FIGURE 41

Alignment of RT Domains from Telomerase Catalytic Subunits.

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                                Motif O
S.p. Tez1p (429). WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIW ... (35)...
S.c. Est2p (366). WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ... (35)...
E.a. p123 (441). WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW ... (35)...
      *          *** **          * * *

      Motif 1      Motif 2      K
      p hh h K      hr h      R
S.p. Tez1p AVIRLLPKK--NTFRLITN-LRKRF ... (61)...
S.c. Est2p SKMRIIPKKSNNEFRIIAIPCRGAD ... (62)...
E.a. p123 GKLRLIPKK--TTFRPIMTFNKKIV ... (61)...
      * ***      ** *

      Motif 3(A) AF
      h hDh GY h
S.p. Tez1p KKYFVRIDIKSCYDRIKQDLMFRIVK ... (89)...
S.c. Est2p ELYFMKFDVKSCYDSIPRMECMRILK ... (75)...
E.a. p123 KLFFATMDIEKCYDSVNREKLSTFLK ... (107)...
      * * ***      *

      Motif 4(B')
      hPQG pP hh h
S.p. Tez1p YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ... (6)...
S.c. Est2p YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF ... (8)...
E.a. p123 YKQTKGIPQGLCVSSILSSFYATLEESSLGF ... (14)...
      * * ** *      * *

      Y Motif 5(C)      Motif 6(D)
      h F DDhhh      Gh h cK h
S.p. Tez1p VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLKTVINFENS . (205)
S.c. Est2p LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAPANRDKILAVSSQS . (173)
E.a. p123 LLMRLTDDYLLITTQENNAVLFIKLINVSRENGFKFNMKKLQTSFPLS . (209)
      ** * *          * *

```

FIGURE 42

A

Sp\_Tip1p 1 .....MTEHHTPKSRILRFLENQVYVLCY 24  
Sc\_Est2p 1 .....MTEHHTPKSRILRFLENQVYVLCY 24  
Ea\_p123 1 MEVDVQDQADNNGHNSALKTCGEEIKETVSVW 25

Sp\_Tip1p 26 LNDYVOLVLRGSPA S SNICERLRSDVQTSFS 27  
Sc\_Est2p 26 LNDYVOLVLRGSPA S SNICERLRSDVQTSFS 27  
Ea\_p123 26 LNDYVOLVLRGSPA S SNICERLRSDVQTSFS 27

Sp\_Tip1p 34 FHLSTYVQFDKPDQGVQSSPKCSQSELAN 40  
Sc\_Est2p 34 FHLSTYVQFDKPDQGVQSSPKCSQSELAN 40  
Ea\_p123 34 FHLSTYVQFDKPDQGVQSSPKCSQSELAN 40

Sp\_Tip1p 51 VVKOMFDSFERRR-LLNKKFSMMHEDFRAMH 122  
Sc\_Est2p 51 VVKOMFDSFERRR-LLNKKFSMMHEDFRAMH 122  
Ea\_p123 51 VVKOMFDSFERRR-LLNKKFSMMHEDFRAMH 122

Sp\_Tip1p 123 VNOVQNDVSTFPNLYSILESKNQLLLEI 155  
Sc\_Est2p 123 VNOVQNDVSTFPNLYSILESKNQLLLEI 155  
Ea\_p123 123 VNOVQNDVSTFPNLYSILESKNQLLLEI 155

Sp\_Tip1p 156 SDAMHYLSKQSIIEALPDNDYLIISIPLEKN 165  
Sc\_Est2p 156 SDAMHYLSKQSIIEALPDNDYLIISIPLEKN 165  
Ea\_p123 156 SDAMHYLSKQSIIEALPDNDYLIISIPLEKN 165

Sp\_Tip1p 199 NVFEETVSKKRTIETSIQN-KSARKE 218  
Sc\_Est2p 199 NVFEETVSKKRTIETSIQN-KSARKE 218  
Ea\_p123 199 NVFEETVSKKRTIETSIQN-KSARKE 218

Sp\_Tip1p 219 WNSISIRFSIFRYSYKIFRSDYFLHLICD 251  
Sc\_Est2p 219 WNSISIRFSIFRYSYKIFRSDYFLHLICD 251  
Ea\_p123 219 WNSISIRFSIFRYSYKIFRSDYFLHLICD 251

Sp\_Tip1p 252 NTVHMWLOWIFRQGLINAFQVKOLHXYPL 264  
Sc\_Est2p 252 NTVHMWLOWIFRQGLINAFQVKOLHXYPL 264  
Ea\_p123 252 NTVHMWLOWIFRQGLINAFQVKOLHXYPL 264

Sp\_Tip1p 266 VS-OSTVVPKRLKLVPLIEQAKRLHRS 313  
Sc\_Est2p 266 VS-OSTVVPKRLKLVPLIEQAKRLHRS 313  
Ea\_p123 266 VS-OSTVVPKRLKLVPLIEQAKRLHRS 313

Sp\_Tip1p 314 LSKVYNNHYID-THDDKILSYSLKPNQ 342  
Sc\_Est2p 314 LSKVYNNHYID-THDDKILSYSLKPNQ 342  
Ea\_p123 314 LSKVYNNHYID-THDDKILSYSLKPNQ 342

Sp\_Tip1p 343 WQNRJFEIIL-DLETFLKSYVESPLHYMS 362  
Sc\_Est2p 343 WQNRJFEIIL-DLETFLKSYVESPLHYMS 362  
Ea\_p123 343 WQNRJFEIIL-DLETFLKSYVESPLHYMS 362

Sp\_Tip1p 366 HNKISIEILVLQKRSNAKMLSDFKRKIFA 425  
Sc\_Est2p 366 HNKISIEILVLQKRSNAKMLSDFKRKIFA 425  
Ea\_p123 366 HNKISIEILVLQKRSNAKMLSDFKRKIFA 425

Sp\_Tip1p 426 EFIVLYNSFIPILOS-SSDLNRTV 456  
Sc\_Est2p 426 EFIVLYNSFIPILOS-SSDLNRTV 456  
Ea\_p123 426 EFIVLYNSFIPILOS-SSDLNRTV 456

Sp\_Tip1p 456 FKKDIKLLCRPFTSMKMEAFKINENVRMD 461  
Sc\_Est2p 456 FKKDIKLLCRPFTSMKMEAFKINENVRMD 461  
Ea\_p123 456 FKKDIKLLCRPFTSMKMEAFKINENVRMD 461

Sp\_Tip1p 492 TOKTTLPPAVILL-NTLTLNLRKFL 522  
Sc\_Est2p 492 TOKTTLPPAVILL-NTLTLNLRKFL 522  
Ea\_p123 492 TOKTTLPPAVILL-NTLTLNLRKFL 522

Sp\_Tip1p 523 IKMOSNKKMLVSTNQLTRPVASIKHIE 562  
Sc\_Est2p 523 IKMOSNKKMLVSTNQLTRPVASIKHIE 562  
Ea\_p123 523 IKMOSNKKMLVSTNQLTRPVASIKHIE 562

Sp\_Tip1p 563 ESSQIPFNLEVMYKLLTKDHRMFAR-KK 584  
Sc\_Est2p 563 ESSQIPFNLEVMYKLLTKDHRMFAR-KK 584  
Ea\_p123 563 ESSQIPFNLEVMYKLLTKDHRMFAR-KK 584

Sp\_Tip1p 586 VYRIKKSRIKODLMFRIVKLLKDP 616  
Sc\_Est2p 586 VYRIKKSRIKODLMFRIVKLLKDP 616  
Ea\_p123 586 VYRIKKSRIKODLMFRIVKLLKDP 616

Sp\_Tip1p 617 VIRKYATIHATSDRATN- 624  
Sc\_Est2p 617 VIRKYATIHATSDRATN- 624  
Ea\_p123 617 VIRKYATIHATSDRATN- 624

Sp\_Tip1p 636 FVSEAFSYFDMVPFEKVLLS-MKTSO 665  
Sc\_Est2p 636 FVSEAFSYFDMVPFEKVLLS-MKTSO 665  
Ea\_p123 636 FVSEAFSYFDMVPFEKVLLS-MKTSO 665

Sp\_Tip1p 666 FVSEAFSYFDMVPFEKVLLS-MKTSO 665  
Sc\_Est2p 666 FVSEAFSYFDMVPFEKVLLS-MKTSO 665  
Ea\_p123 666 FVSEAFSYFDMVPFEKVLLS-MKTSO 665

Sp\_Tip1p 696 LKVVIP-SILSFLCHYMEDIDEYLS 721  
Sc\_Est2p 696 LKVVIP-SILSFLCHYMEDIDEYLS 721  
Ea\_p123 696 LKVVIP-SILSFLCHYMEDIDEYLS 721

Sp\_Tip1p 722 KKG-SVLLRVVFFVYNNKDKAK 756  
Sc\_Est2p 722 KKG-SVLLRVVFFVYNNKDKAK 756  
Ea\_p123 722 KKG-SVLLRVVFFVYNNKDKAK 756

Sp\_Tip1p 757 FLNLSLRQFEKNHFSYSLTYVINEN 785  
Sc\_Est2p 757 FLNLSLRQFEKNHFSYSLTYVINEN 785  
Ea\_p123 757 FLNLSLRQFEKNHFSYSLTYVINEN 785

Sp\_Tip1p 787 LNNHTFESKKRPFFVYNNKDKAK 815  
Sc\_Est2p 787 LNNHTFESKKRPFFVYNNKDKAK 815  
Ea\_p123 787 LNNHTFESKKRPFFVYNNKDKAK 815

Sp\_Tip1p 817 ACCKIDEALFNSTSVETKHMGSFFYLRSS 848  
Sc\_Est2p 817 ACCKIDEALFNSTSVETKHMGSFFYLRSS 848  
Ea\_p123 817 ACCKIDEALFNSTSVETKHMGSFFYLRSS 848

Sp\_Tip1p 850 ASFAOVFIDITHNSKFNSCCNIRLYGSMCMR 882  
Sc\_Est2p 850 ASFAOVFIDITHNSKFNSCCNIRLYGSMCMR 882  
Ea\_p123 850 ASFAOVFIDITHNSKFNSCCNIRLYGSMCMR 882

Sp\_Tip1p 883 AQAYLKR-IFIPORMFIDLLNVIRK 915  
Sc\_Est2p 883 AQAYLKR-IFIPORMFIDLLNVIRK 915  
Ea\_p123 883 AQAYLKR-IFIPORMFIDLLNVIRK 915

Sp\_Tip1p 916 LAEILQYTSRRFLSSAEVKKWFLQGMROCKPS 946  
Sc\_Est2p 916 LAEILQYTSRRFLSSAEVKKWFLQGMROCKPS 946  
Ea\_p123 916 LAEILQYTSRRFLSSAEVKKWFLQGMROCKPS 946

Sp\_Tip1p 949 FKYPGCEQLIYQSLTDILPLRPVROVL 981  
Sc\_Est2p 949 FKYPGCEQLIYQSLTDILPLRPVROVL 981  
Ea\_p123 949 FKYPGCEQLIYQSLTDILPLRPVROVL 981

Sp\_Tip1p 982 LHRRIAD- 986  
Sc\_Est2p 982 LHRRIAD- 986  
Ea\_p123 982 LHRRIAD- 986

B

Sp\_Tip1p 1 .....MTEHHTPKSRILRFLENQVYVLCY 24  
Sc\_Est2p 1 .....MTEHHTPKSRILRFLENQVYVLCY 24  
Ea\_p123 1 MEVDVQDQADNNGHNSALKTCGEEIKETVSVW 25

Sp\_Tip1p 26 LNDYVOLVLRGSPA S SNICERLRSDVQTSFS 27  
Sc\_Est2p 26 LNDYVOLVLRGSPA S SNICERLRSDVQTSFS 27  
Ea\_p123 26 LNDYVOLVLRGSPA S SNICERLRSDVQTSFS 27

Sp\_Tip1p 34 FHLSTYVQFDKPDQGVQSSPKCSQSELAN 40  
Sc\_Est2p 34 FHLSTYVQFDKPDQGVQSSPKCSQSELAN 40  
Ea\_p123 34 FHLSTYVQFDKPDQGVQSSPKCSQSELAN 40

Sp\_Tip1p 51 VVKOMFDSFERRR-LLNKKFSMMHEDFRAMH 122  
Sc\_Est2p 51 VVKOMFDSFERRR-LLNKKFSMMHEDFRAMH 122  
Ea\_p123 51 VVKOMFDSFERRR-LLNKKFSMMHEDFRAMH 122

Sp\_Tip1p 123 VNOVQNDVSTFPNLYSILESKNQLLLEI 155  
Sc\_Est2p 123 VNOVQNDVSTFPNLYSILESKNQLLLEI 155  
Ea\_p123 123 VNOVQNDVSTFPNLYSILESKNQLLLEI 155

Sp\_Tip1p 156 SDAMHYLSKQSIIEALPDNDYLIISIPLEKN 165  
Sc\_Est2p 156 SDAMHYLSKQSIIEALPDNDYLIISIPLEKN 165  
Ea\_p123 156 SDAMHYLSKQSIIEALPDNDYLIISIPLEKN 165

Sp\_Tip1p 199 NVFEETVSKKRTIETSIQN-KSARKE 218  
Sc\_Est2p 199 NVFEETVSKKRTIETSIQN-KSARKE 218  
Ea\_p123 199 NVFEETVSKKRTIETSIQN-KSARKE 218

Sp\_Tip1p 219 WNSISIRFSIFRYSYKIFRSDYFLHLICD 251  
Sc\_Est2p 219 WNSISIRFSIFRYSYKIFRSDYFLHLICD 251  
Ea\_p123 219 WNSISIRFSIFRYSYKIFRSDYFLHLICD 251

Sp\_Tip1p 252 NTVHMWLOWIFRQGLINAFQVKOLHXYPL 264  
Sc\_Est2p 252 NTVHMWLOWIFRQGLINAFQVKOLHXYPL 264  
Ea\_p123 252 NTVHMWLOWIFRQGLINAFQVKOLHXYPL 264

Sp\_Tip1p 266 VS-OSTVVPKRLKLVPLIEQAKRLHRS 313  
Sc\_Est2p 266 VS-OSTVVPKRLKLVPLIEQAKRLHRS 313  
Ea\_p123 266 VS-OSTVVPKRLKLVPLIEQAKRLHRS 313

Sp\_Tip1p 314 LSKVYNNHYID-THDDKILSYSLKPNQ 342  
Sc\_Est2p 314 LSKVYNNHYID-THDDKILSYSLKPNQ 342  
Ea\_p123 314 LSKVYNNHYID-THDDKILSYSLKPNQ 342

Sp\_Tip1p 343 WQNRJFEIIL-DLETFLKSYVESPLHYMS 362  
Sc\_Est2p 343 WQNRJFEIIL-DLETFLKSYVESPLHYMS 362  
Ea\_p123 343 WQNRJFEIIL-DLETFLKSYVESPLHYMS 362

Sp\_Tip1p 366 HNKISIEILVLQKRSNAKMLSDFKRKIFA 425  
Sc\_Est2p 366 HNKISIEILVLQKRSNAKMLSDFKRKIFA 425  
Ea\_p123 366 HNKISIEILVLQKRSNAKMLSDFKRKIFA 425

Sp\_Tip1p 426 EFIVLYNSFIPILOS-SSDLNRTV 456  
Sc\_Est2p 426 EFIVLYNSFIPILOS-SSDLNRTV 456  
Ea\_p123 426 EFIVLYNSFIPILOS-SSDLNRTV 456

Sp\_Tip1p 456 FKKDIKLLCRPFTSMKMEAFKINENVRMD 461  
Sc\_Est2p 456 FKKDIKLLCRPFTSMKMEAFKINENVRMD 461  
Ea\_p123 456 FKKDIKLLCRPFTSMKMEAFKINENVRMD 461

Sp\_Tip1p 492 TOKTTLPPAVILL-NTLTLNLRKFL 522  
Sc\_Est2p 492 TOKTTLPPAVILL-NTLTLNLRKFL 522  
Ea\_p123 492 TOKTTLPPAVILL-NTLTLNLRKFL 522

Sp\_Tip1p 523 IKMOSNKKMLVSTNQLTRPVASIKHIE 562  
Sc\_Est2p 523 IKMOSNKKMLVSTNQLTRPVASIKHIE 562  
Ea\_p123 523 IKMOSNKKMLVSTNQLTRPVASIKHIE 562

Sp\_Tip1p 563 ESSQIPFNLEVMYKLLTKDHRMFAR-KK 584  
Sc\_Est2p 563 ESSQIPFNLEVMYKLLTKDHRMFAR-KK 584  
Ea\_p123 563 ESSQIPFNLEVMYKLLTKDHRMFAR-KK 584

Sp\_Tip1p 586 VYRIKKSRIKODLMFRIVKLLKDP 616  
Sc\_Est2p 586 VYRIKKSRIKODLMFRIVKLLKDP 616  
Ea\_p123 586 VYRIKKSRIKODLMFRIVKLLKDP 616

Sp\_Tip1p 617 VIRKYATIHATSDRATN- 624  
Sc\_Est2p 617 VIRKYATIHATSDRATN- 624  
Ea\_p123 617 VIRKYATIHATSDRATN- 624

Sp\_Tip1p 636 FVSEAFSYFDMVPFEKVLLS-MKTSO 665  
Sc\_Est2p 636 FVSEAFSYFDMVPFEKVLLS-MKTSO 665  
Ea\_p123 636 FVSEAFSYFDMVPFEKVLLS-MKTSO 665

Sp\_Tip1p 666 FVSEAFSYFDMVPFEKVLLS-MKTSO 665  
Sc\_Est2p 666 FVSEAFSYFDMVPFEKVLLS-MKTSO 665  
Ea\_p123 666 FVSEAFSYFDMVPFEKVLLS-MKTSO 665

Sp\_Tip1p 696 LKVVIP-SILSFLCHYMEDIDEYLS 721  
Sc\_Est2p 696 LKVVIP-SILSFLCHYMEDIDEYLS 721  
Ea\_p123 696 LKVVIP-SILSFLCHYMEDIDEYLS 721

Sp\_Tip1p 722 KKG-SVLLRVVFFVYNNKDKAK 756  
Sc\_Est2p 722 KKG-SVLLRVVFFVYNNKDKAK 756  
Ea\_p123 722 KKG-SVLLRVVFFVYNNKDKAK 756

Sp\_Tip1p 757 FLNLSLRQFEKNHFSYSLTYVINEN 785  
Sc\_Est2p 757 FLNLSLRQFEKNHFSYSLTYVINEN 785  
Ea\_p123 757 FLNLSLRQFEKNHFSYSLTYVINEN 785

Sp\_Tip1p 787 LNNHTFESKKRPFFVYNNKDKAK 815  
Sc\_Est2p 787 LNNHTFESKKRPFFVYNNKDKAK 815  
Ea\_p123 787 LNNHTFESKKRPFFVYNNKDKAK 815

Sp\_Tip1p 817 ACCKIDEALFNSTSVETKHMGSFFYLRSS 848  
Sc\_Est2p 817 ACCKIDEALFNSTSVETKHMGSFFYLRSS 848  
Ea\_p123 817 ACCKIDEALFNSTSVETKHMGSFFYLRSS 848

Sp\_Tip1p 850 ASFAOVFIDITHNSKFNSCCNIRLYGSMCMR 882  
Sc\_Est2p 850 ASFAOVFIDITHNSKFNSCCNIRLYGSMCMR 882  
Ea\_p123 850 ASFAOVFIDITHNSKFNSCCNIRLYGSMCMR 882

Sp\_Tip1p 883 AQAYLKR-IFIPORMFIDLLNVIRK 915  
Sc\_Est2p 883 AQAYLKR-IFIPORMFIDLLNVIRK 915  
Ea\_p123 883 AQAYLKR-IFIPORMFIDLLNVIRK 915

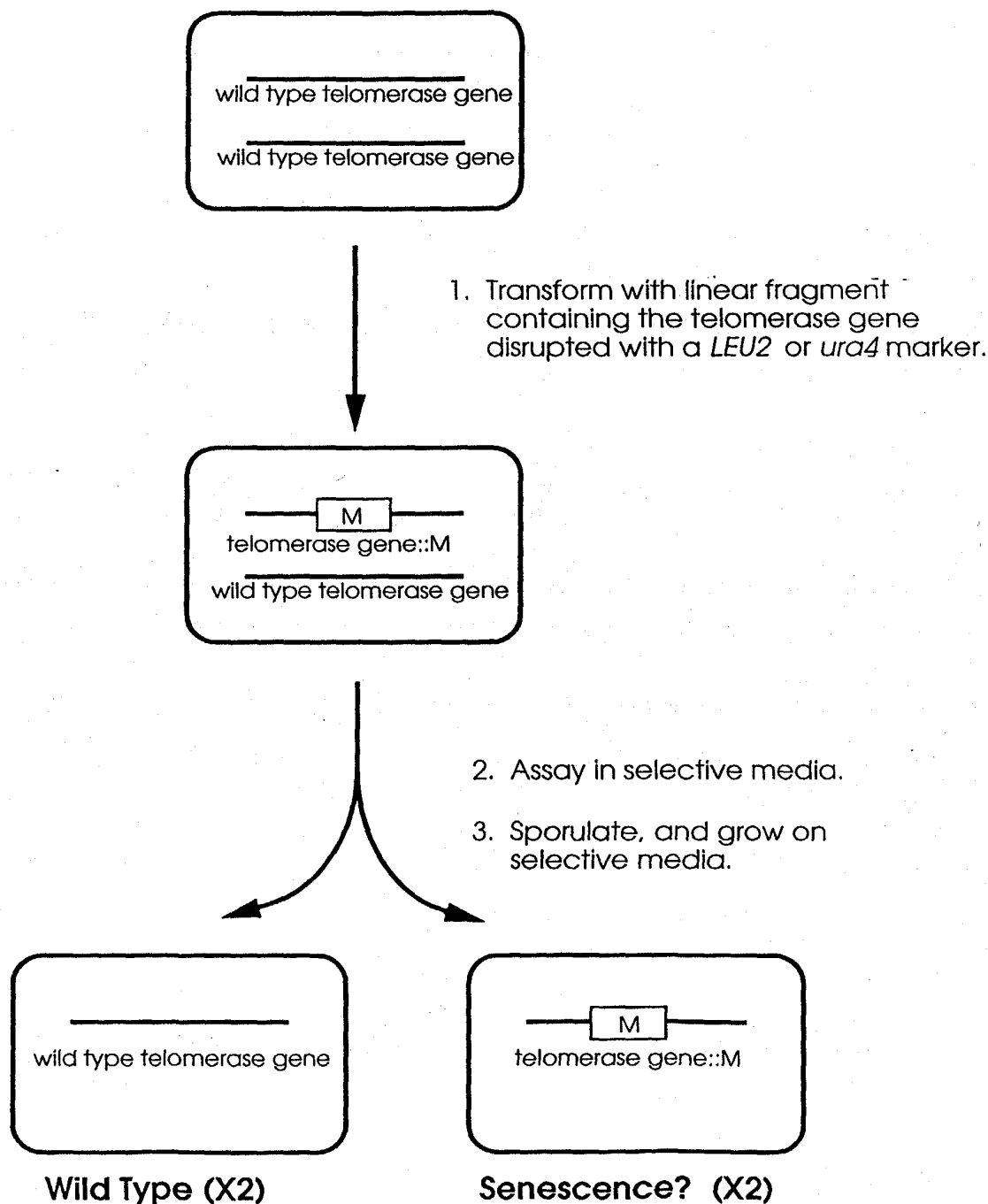
Sp\_Tip1p 916 LAEILQYTSRRFLSSAEVKKWFLQGMROCKPS 946  
Sc\_Est2p 916 LAEILQYTSRRFLSSAEVKKWFLQGMROCKPS 946  
Ea\_p123 916 LAEILQYTSRRFLSSAEVKKWFLQGMROCKPS 946

Sp\_Tip1p 949 FKYPGCEQLIYQSLTDILPLRPVROVL 981  
Sc\_Est2p 949 FKYPGCEQLIYQSLTDILPLRPVROVL 981  
Ea\_p123 949 FKYPGCEQLIYQSLTDILPLRPVROVL 981

Sp\_Tip1p 982 LHRRIAD- 986  
Sc\_Est2p 982 LHRRIAD- 986  
Ea\_p123 982 LHRRIAD- 986

FIGURE 43

# Disruption strategy for the putative telomerase genes.



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)



FIGURE 44

An Example of Confirmation of *tez1* disruption By PCR

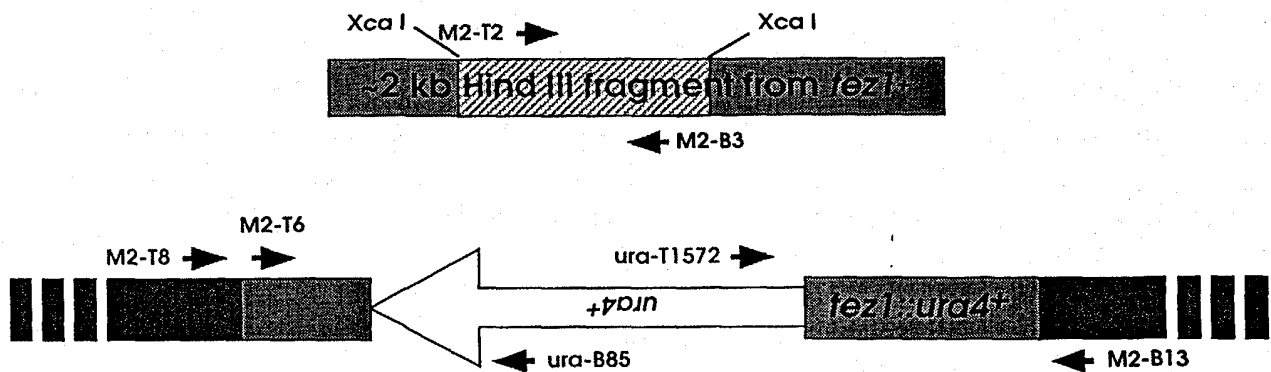
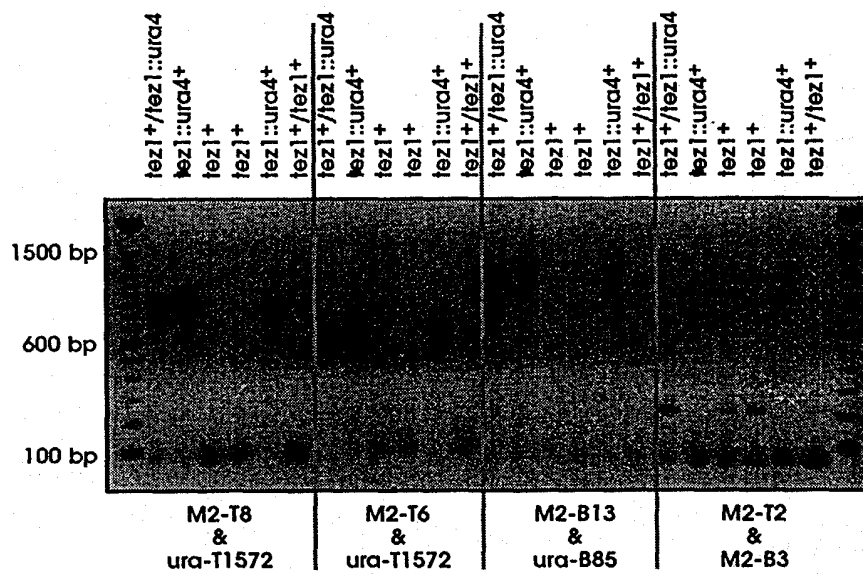


FIGURE 45

*Tez1* disruption causes progressive shortening of telomeres in *S. pombe*

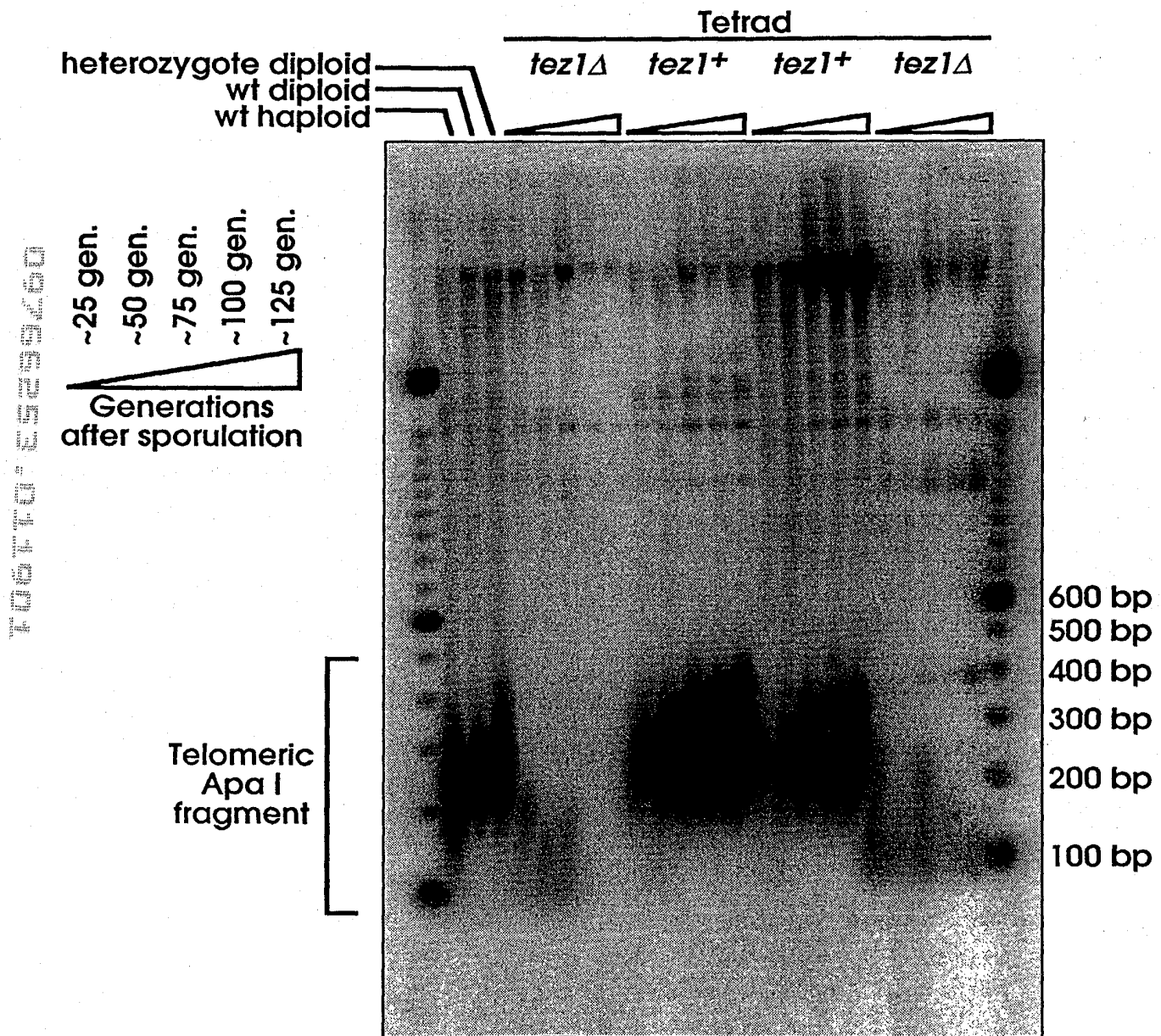


FIGURE 46

1 ggtaccgatttacttttcctttcttcataagctaattgcttctcogaacgctcctaaatctctggaaatatttttacaaga 80  
81 actcaataacaataccaagtcaaattccaatatgaagggtgttatttagtgatcgataatattttctatttttatcggtcggtta 160  
161 ccaagtataaggacaaaaagaacaacttccttccccctaaagacttttacttttattaatttacttttcaaataatatttcg 240  
241 gggttcgcttacttttaacgtggtactgttttagctgctacttctagccaaccgctgtttctaccccgctcattggatat 320  
321 agctcttggagtagctcacagaaatccttacaatcttctgatgagactatattagattcattacagtcggtgcatattc 400  
401 ttaacatggagccttacacttttagatgagtcacgtcgcatgatggagtatttggtatcatccaacggttgacctgaaaag 480  
481 gttgataattatttgcaaaatcatgtccttagtggtggtgaatccgcgaaagttttttgatgcttgcacacgtctagcatg 560  
561 attgagatattcaaaaaatttctatccactacaactcctttaacgcggtttttatttttctattttctattctcatgttggt 640  
641 ccaaatatgtatcatctcgtattaggcttttttccggttttactcctggaatcgtaaccttttctactattccccctaata 720  
721 ataactctaaattagtttctgcttataattgatagtagtagaaagattgggtgattctactcgtgtaattgttattagtttaa 800  
801 gatactttgcaaaacatttatttagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc 880  
881 actattttatttaaacggttatgatcagtaggacactttgcatatatatagttatgcttaatgggttacttgtaacttgc 958

959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018  
1 M T E H H T P K S R I L R F L E N Q Y V 20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078  
21 Y L C T L N D Y V Q L V L R G S P A S S 40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT 1138  
41 Y S N I C E R L R S D V Q T S F S I F L 60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198  
61 H S T V V G F D S K P D E G V Q F S S P 80

FIGURE 46 (cont.)

1199	AAA TGC TCA CAG TCA GAG	gtatatatatttttgttttgatttttttctattcgggatagctaatatatgggcag	1272
81	K C S Q S E		86
1273	CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA		1332
87	L I A N V V K Q M F D E S F E R R R N L		106
1333	CTG ATG AAA GGG TTT TCC ATG	gtaagggtatttctaattgtgaaatatttacctgcaattactgtttcaaagaga	1405
107	L M K G F S M		113
1406	ttgtattttaaccgataaag	AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT	1469
114		N H E D F R A M H V N G V Q N	128
1470	GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA		1529
129	D L V S T F P N Y L I S I L E S K N W Q		148
1530	CTT TTG TTA GAA AT	gtaaataccggttaagatgttgcgcactttgaacaagactgacaagtatag T ATC GGC	1601
149	L L L E I		I G 155
1602	AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC		1661
156	S D A M H Y L L S K G S I F E A L P N D		175
1662	AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG		1721
176	N Y L Q I S G I P L F K N N V F E E T V		195
1722	TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA		1781
196	S K K R K R T I E T S I T Q N K S A R K		215
1782	GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT		1841
216	E V S W N S I S I S R F S I F Y R S S Y		235
1842	AAG AAG TTT AAG CAA G	gtaactaataactgttatccttcataactaatttttag AT CTA TAT TTT AAC	
1907			
236	K K F K Q D		L Y F N 245
1908	TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG		1967
246	L H S I C D R N T V H M W L Q W I F P R		265
1968	CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA		2027
266	Q F G L I N A F Q V K Q L H K V I P L V		285
2028	TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA		2087
286	S Q S T V V P K R L L K V Y P L I E Q T		305
2088	GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT		2147
306	A K R L H R I S L S K V Y N H Y C P Y I		325
2148	GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG		2207
326	D T H D D E K I L S Y S L K P N Q V F A		345
2208	TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA		2267
346	F L R S I L V R V F P K L I W G N Q R I		365
2268	TTT GAG ATA ATA TTA AAA G	gtattgtataaaaatttattaccactaacgattttaccag AC CTC GAA ACT	2336
366	F E I I L K D		L E T 375

FIGURE 46 (cont.)

2337	TTC	TTG	AAA	TTA	TCG	AGA	TAC	GAG	TCT	TTT	AGT	TTA	CAT	TAT	TTA	ATG	AGT	AAC	ATA	AAG	2396																
376	F	L	K	L	S	R	Y	E	S	F	S	L	H	Y	L	M	S	N	I	K	395																
2397	gtaatatgccaaatttttttaccattaattaacaatcag																			ATT	TCA	GAA	ATT	GAA	TGG	CTA	GTC	CTT	GGA	2465							
396																				I	S	E	I	E	W	L	V	L	G	405							
2466	AAA	AGG	TCA	AAT	GCG	AAA	ATG	TGC	TTA	AGT	GAT	TTT	GAG	AAA	CGC	AAG	CAA	ATA	TTT	GCG	2525																
406	K	R	S	N	A	K	M	C	L	S	D	F	E	K	R	K	Q	I	F	A	425																
2526	GAA	TTC	ATC	TAC	TGG	CTA	TAC	AAT	TCG	TTT	ATA	ATA	CCT	ATT	TTA	CAA	TCT	TTT	TTT	TAT	2585																
426	E	F	I	Y	W	L	Y	N	S	F	I	I	P	I	L	Q	S	F	F	Y	445																
2586	ATC	ACT	GAA	TCA	AGT	GAT	TTA	CGA	AAT	CGA	ACT	GTT	TAT	TTT	AGA	AAA	GAT	ATT	TGG	AAA	2645																
446	I	T	E	S	S	D	L	R	N	R	T	V	Y	F	R	K	D	I	W	K	465																
2646	CTC	TTG	TGC	CGA	CCC	TTT	ATT	ACA	TCA	ATG	AAA	ATG	GAA	GCG	TTT	GAA	AAA-ATA	AAC	GAG	2705																	
466	L	L	C	R	P	F	I	T	S	M	K	M	E	A	F	E	K	I	N	E	485																
2706	gtattttaaagtattttttgcaaaaagctaataattttcag																			AAC	AAT	GTT	AGG	ATG	GAT	ACT	CAG	AAA	ACT	2775							
486																				N	N	V	R	M	D	T	Q	K	T	495							
2776	ACT	TTG	CCT	CCA	GCA	GTT	ATT	CGT	CTA	TTA	CCT	AAG	AAG	AAT	ACC	TTT	CGT	CTC	ATT	ACG	2835																
496	T	L	P	P	A	V	I	R	L	L	P	K	K	N	T	F	R	L	I	T	515																
2836	AAT	TTA	AGA	AAA	AGA	TTC	TTA	ATA	AAG	gtattaatttttggcatcaatgtactttactttctaatactatta											2906																
516	N	L	R	K	R	F	L	I	K												524																
2907	ttagcag	ATG	GGT	TCA	AAC	AAA	AAA	ATG	TTA	GTC	AGT	ACG	AAC	CAA	ACT	TTA	CGA	CCT	GTG	2967																	
525		M	G	S	N	K	K	M	L	V	S	T	N	Q	T	L	R	P	V	542																	
2968	GCA	TCG	ATA	CTG	AAA	CAT	TTA	ATC	AAT	GAA	GAA	AGT	AGT	GGT	ATT	CCA	TTT	AAC	TTG	GAG	3027																
543	A	S	I	L	K	H	L	I	N	E	E	S	S	G	I	P	F	N	L	E	562																
3028	GTT	TAC	ATG	AAG	CTT	CTT	ACT	TTT	AAG	AAG	GAT	CTT	CTT	AAG	CAC	CGA	ATG	TTT	GG	gtaat	3088																
563	V	Y	M	K	L	L	T	F	K	K	D	L	L	K	H	R	M	F	G		581																
3089	tatataatgcgcgattcctcattattaattttgcag																			G	CGT	AAG	AAG	TAT	TTT	GTA	CGG	ATA	GAT	ATA	3155						
582																				R	K	K	Y	F	V	R	I	D	I	591							
3156	AAA	TCC	TGT	TAT	GAT	CGA	ATA	AAG	CAA	GAT	TTG	ATG	TTT	CGG	ATT	GTT	AAA	AAG	AAA	CTC	3215																
592	K	S	C	Y	D	R	I	K	Q	D	L	M	F	R	I	V	K	K	K	L	611																
3216	AAG	GAT	CCC	GAA	TTT	GTA	ATT	CGA	AAG	TAT	GCA	ACC	ATA	CAT	GCA	ACA	AGT	GAC	CGA	GCT	3275																
612	K	D	P	E	F	V	I	R	K	Y	A	T	I	H	A	T	S	D	R	A	631																
3276	ACA	AAA	AAC	TTT	GTT	AGT	GAG	GCG	TTT	TCC	TAT	T	gtaagtttatttttttattggaattttttaacaa											3343													
632	T	K	N	F	V	S	E	A	F	S	Y	F												643													
3344	attcttttttag																			TT	GAT	ATG	GTG	CCT	TTT	GAA	AAA	GTC	GTG	CAG	TTA	CTT	TCT	ATG	AAA	ACA	3405
644																					D	M	V	P	F	E	K	V	V	Q	L	L	S	M	K	T	659
3406	TCA	GAT	ACT	TTG	TTT	GTT	GAT	TTT	GTG	GAT	TAT	TGG	ACC	AAA	AGT	TCT	TCT	GAA	ATT	TTT	3465																
660	S	D	T	L	F	V	D	F	V	D	Y	W	T	K	S	S	S	E	I	F	679																
3466	AAA	ATG	CTC	AAG	GAA	CAT	CTC	TCT	GGA	CAC	ATT	GTT	AAG	gtataccaattgttgaattgtaataaca											3532												
680	K	M	L	K	E	H	L	S	G	H	I	V	K												692												

**FIGURE 46 (cont.)**

3533	cta	aatgaa	actag	ATA	GGA	AAT	TCT	CAA	TAC	CTT	CAA	AAA	GTT	GGT	ATC	CCT	CAG	GGC	TCA	3593	
693	I	G	N	S	Q	Y	L	Q	K	V	G	I	P	Q	G	S				708	
3594	ATT	CTG	TCA	TCT	TTT	TTG	TGT	CAT	TTC	TAT	ATG	GAA	GAT	TTG	ATT	GAT	GAA	TAC	CTA	TCG	3653
709	I	L	S	S	F	L	C	H	F	Y	M	E	D	L	I	D	E	Y	L	S	728
3654	TTT	ACG	AAA	AAG	AAA	GGA	TCA	GTG	TTG	TTA	CGA	GTA	GTC	GAC	GAT	TTC	CTC	TTT	ATA	ACA	3713
729	F	T	K	K	K	G	S	V	L	L	R	V	V	D	D	F	L	F	I	T	748
3714	GTT	AAT	AAA	AAG	GAT	GCA	AAA	AAA	TTT	TTG	AAT	TTA	TCT	TTA	AGA	G	gtgagttgctgtcattcc				3777
749	V	N	K	K	D	A	K	K	F	L	N	L	S	L	R	G					764
3778	taagttcta	accg	ttgaag	GA	TTT	GAG	AAA	CAC	AAT	TTT	TCT	ACG	AGC	CTG	GAG	AAA	ACA	GTA			3840
765					F	E	K	H	N	F	S	T	S	L	E	K	T	V			778
3841	ATA	AAC	TTT	GAA	AAT	AGT	AAT	GGG	ATA	ATA	AAC	AAT	ACT	TTT	TTT	AAT	GAA	AGC	AAG	AAA	3900
779	I	N	F	E	N	S	N	G	I	I	N	N	T	F	F	N	E	S	K	K	798
3901	AGA	ATG	CCA	TTC	TTC	GGT	TTC	TCT	GTG	AAC	ATG	AGG	TCT	CTT	GAT	ACA	TTG	TTA	GCA	TGT	3960
799	R	M	P	F	F	G	F	S	V	N	M	R	S	L	D	T	L	L	A	C	818
3961	CCT	AAA	ATT	GAT	GAA	GCC	TTA	TTT	AAC	TCT	ACA	TCT	GTA	GAG	CTG	ACG	AAA	CAT	ATG	GGG	4020
819	P	K	I	D	E	A	L	F	N	S	T	S	V	E	L	T	K	H	M	G	838
4021	AAA	TCT	TTT	TTT	TAC	AAA	ATT	CTA	AG	gtatactgtgtaactgaataatagctgacaaataatcag	A	TCG									4089
839	K	S	F	F	Y	K	I	L	R												848
4090	AGC	CTT	GCA	TCC	TTT	GCA	CAA	GTA	TTT	ATT	GAC	ATT	ACC	CAC	AAT	TCA	AAA	TTC	AAT	TCT	4149
849	S	L	A	S	F	A	Q	V	F	I	D	I	T	H	N	S	K	F	N	S	868
4150	TGC	TGC	AAT	ATA	TAT	AGG	CTA	GGA	TAC	TCT	ATG	TGT	ATG	AGA	GCA	CAA	GCA	TAC	TTA	AAA	4209
869	C	C	N	I	Y	R	L	G	Y	S	M	C	M	R	A	Q	A	Y	L	K	888
4210	AGG	ATG	AAG	GAT	ATA	TTT	ATT	CCC	CAA	AGA	ATG	TTC	ATA	ACG	G	gtgagtacttatttttaactaga					4274
889	R	M	K	D	I	F	I	P	Q	R	M	F	I	T	D						903
4275	aaagtcatta	attaac	cttag	AT	CTT	TTG	AAT	GTT	ATT	GGA	AGA	AAA	ATT	TGG	AAA	AAG	TTG	GCC			4339
904					L	L	N	V	I	G	R	K	I	W	K	K	L	A			917
4340	GAA	ATA	TTA	GGA	TAT	ACG	AGT	AGG	CGT	TTC	TTG	TCC	TCT	GCA	GAA	GTC	AAA	TG	gtacgtgtc		4401
918	E	I	L	G	Y	T	S	R	R	F	L	S	S	A	E	V	K	W			935
4402	ggtctcgagacttcag	caatattgacacatcag	G	CTT	TTT	TGT	CTT	GGA	ATG	AGA	GAT	GGT	TTG	AAA							4468
936					L	F	C	L	G	M	R	D	G	L	K						946
4469	CCC	TCT	TTC	AAA	TAT	C															

**FIGURE 46 (cont.)**

4666	gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagtttttgattgacttgtct	4745
4746	ttatcctttatactttttaagaaagattgacagtggttgctgactactgccacatgccattaaacgggagtggttaaaca	4825
4826	ttaaaagtaatacatgaggctaatactccttttcatttagaataaggaaagtgggttttctataatgaataatgccgcacta	4905
4906	atgcaaaaaagacgaagattatcttctaacaagggggattaagcatatccgaaggaaaagagagtaataataccagtggt	4985
4986	gttgaagaaagcaaggataaatttggacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc	5065
5066	ccaggttatccatgggtggcggccttgctactgagacgaaaagaaactaaggatagtttgaataactaatagctcattta	5145
5146	atgtcttatataaagggttttgttttttctgacttcaattttgcacgggtgaaaagaaatagtgttaagccattattggat	5225
5226	tccgaaatagccaaatttcttggttctctcaaagcgggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc	5305
5306	tcctgatttaaaggaggaactcttccaccgatgaggaaatggatagcttattcagctgctgaggagaagcctaattttttgc	5385
5386	aaaaaagaaaatacatctgggagacatctcttggaatcagatgcggagagatctccagcggaatccttgatgtcaata	5465
5466	acttctattttctgaaatgtatggtcctactgtcgtcttcgacttctcgtagctctacgcagttaaagtgaccaaaggtacc	5544

[illegible]

FIGURE 47

[illegible]



FIGURE 47 (cont.)

190	thr	tyr	cys	val	arg	arg	tyr	ala	val	val	200	gln	lys	ala	ala	met
	ACG	TAC	TGC	GTG	CGT	CGG	TAT	GCC	GTG	GTC		CAG	AAG	GCC	GCC	ATG
	gly	thr	ser	ala	arg	pro	ser	arg	ala	thr	210	ser	tyr	val	gln	cys
	GGC	ACG	TCC	GCA	AGG	CCT	TCA	AGA	GCC	ACG		TCC	TAC	GTC	CAG	TGC
220	gln	gly	ile	pro	gln	gly	ser	ile	leu	ser	230	thr	leu	leu	cys	ser
	CAG	GGG	ATC	CCG	CAG	GGC	TCC	ATC	CTC	TCC		ACG	CTG	CTC	TGC	AGC
	leu	cys	tyr	gly	asp	met	glu	asn	lys	leu	240	phe	ala	gly	ile	arg
	CTG	TGC	TAC	GGC	GAC	ATG	GAG	AAC	AAG	CTG		TTT	GCG	GGG	ATT	CGG
250	arg	asp	gly	leu	leu	leu	arg	leu	val	asp	260	asp	phe	leu	leu	val
	CGG	GAC	GGG	CTG	CTC	CTG	CGT	TTG	GTG	GAT		GAT	TTC	TTG	TTG	GTG
	thr	pro	his	leu	thr	his	ala	lys	thr	phe	270	leu	arg	thr	leu	val
	ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	ACC	TTC		CTC	AGG	ACC	CTG	GTC
280	arg	gly	val	pro	glu	tyr	gly	cys	val	val	290	asn	leu	arg	lys	thr
	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	GTG		AAC	TTG	CGG	AAG	ACA
	val	val	asn	phe	pro	val	glu	asp	glu	ala	300	leu	gly	gly	thr	ala
	GTG	GTG	AAC	TTC	CCT	GTA	GAA	GAC	GAG	GCC		CTG	GGT	GGC	ACG	GCT
310	phe	val	gln	met	pro	ala	his	gly	leu	phe	320	pro	trp	cys	gly	leu
	TTT	GTT	CAG	ATG	CCG	GCC	CAC	GGC	CTA	TTC		CCC	TGG	TGC	GGC	CTG
	leu	leu	asp	thr	arg	thr	leu	glu	val	gln	330	ser	asp	tyr	ser	ser
	CTG	CTG	GAT	ACC	CGG	ACC	CTG	GAG	GTG	CAG		AGC	GAC	TAC	TCC	AGC
340	tyr	ala	arg	thr	ser	ile	arg	ala	ser	leu	350	thr	phe	asn	arg	gly
	TAT	GCC	CGG	ACC	TCC	ATC	AGA	GCC	AGT	CTC		ACC	TTC	AAC	CGC	GGC
	phe	lys	ala	gly	arg	asn	met	arg	arg	lys	360	leu	phe	gly	val	leu
	TTC	AAG	GCT	GGG	AGG	AAC	ATG	CGT	CGC	AAA		CTC	TTT	GGG	GTC	TTG
370	arg	leu	lys	cys	his	ser	leu	phe	leu	asp	380	leu	gln	val	asn	ser
	CGG	CTG	AAG	TGT	CAC	AGC	CTG	TTT	CTG	GAT		TTG	CAG	GTG	AAC	AGC

FIGURE 47 (cont.)

390  
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln  
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400 410  
ala tyr arg phe his ala cys val leu gln leu pro phe his gln  
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

420  
gln val trp lys asn pro his phe ser cys ala ser ser leu thr  
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430 440  
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp  
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

450  
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly  
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460 470  
arg ala val ala val pro pro ser ile pro ala gln ala asp ser  
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

480  
thr pro cys his leu arg ala thr pro gly val thr gln asp ser  
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490 500  
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys  
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

510  
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp  
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520 530  
his pro gly leu met ala thr arg pro gln pro gly arg glu gln  
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

540  
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly  
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGC

550 560  
arg gly gly pro his pro gly leu his arg trp glu ser glu ala  
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564  
OP  
TGA GTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCGGGCTGAGGC  
CTGAGCGAGTGTCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

**FIGURE 47 (cont.)**

AGGCTGGCGTTTCGGTCCACCCCAGGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACT  
CCCCACATAGGAATAGTCCATCCCCAGATTGCGCATTGTTTACCCTTCGCCCTGCCTTCC  
TTTGCCTTCCACCCCCACCATTGAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG  
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG  
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT  
TTTCAGTTTGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

FIGURE 48

Motif -1  
 Ep p123 ...LVVSLIRCFYVTEQQKSYSKT...  
 Sp Tez1 ...FIIPILQSFFYITESSDLRNRT...  
 Sc Est2 ...LIPKIIQTFFYCTEISSTVTIV...  
 Hs TCP1 ...YVVELLRSSFFYVTETTFQKNRL...  
 consensus FFY TE

Motif 0  
 Ep p123 ...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...  
 Sp Tez1 ...QKTTLPPAVIRLLPKKN--TFLITNLRKRFL...  
 Sc Est2 ...TLSNFNHSKMRIIPKKSNNFRIIAIPCRGAD...  
 Hs TCP1 ...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...  
 consensus R PK RI

Motif A  
 Ep p123 ...PKLFFATMDIEKCYDSVNREKLSTFLK...  
 Sp Tez1 ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...  
 Sc Est2 ...PELYFMKFDVKSCYDSIPRMECMRILK...  
 Hs TCP1 ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...  
 consensus F D YD

Motif B  
 Ep p123 ...NGKFYKQTKGIPQGLCVSSILSSFYYA...  
 Sp Tez1 ...GNSQYLQKVGIPQGSILSSFLCHFyme...  
 Sc Est2 ...EDKCYIREDGLFQGSSLSAPIVDLVYD...  
 Hs TCP1 ...RATSYVQCQGIPQGSILSTLLCSLCYG...  
 consensus G QG S

Motif C  
 Ep p123 ...PNVNLLMRLTDDYLLITTQENN...  
 Sp Tez1 ...KKGSVLLRVVDDFLFITVNKKD...  
 Sc Est2 ...SQDTLILKLADDFLIISTDQQQ...  
 Hs TCP1 ...RRDGLLLRLVDDFLLVTPHLTH...  
 consensus DD L

Motif D  
 Ep p123 ...NVSRENGFKFNMKKL...  
 Sp Tez1 ...LNLSLRGFEKHNFST...  
 Sc Est2 ...KKLAMGGFQKYNKA...  
 Hs TCP1 ...LRTLVRGVPEYGCVV...  
 consensus G